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Sequence:

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AF191212 Mus muscu
AC073459 Homo sapi
AL68383 Mouse DNA
AC142180 Rattus no
AC129766 Rattus no
BV208714 NR43_216
BC009288 Homo sapi
C0727361 Sequence
AX353492 Sequence
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AX67918 H.sapiens m
U7245 Rattus norv
AX66794 Sequence
U01146 Rattus norv
S5374 WURRI-Nur-r
AR177670 Sequence
U01146 Rattus norv
S5374 WURRI-Nur-r
AX177670 Sequence
U08595 Rat nuclear
BC066890 Homo sapi
S77154 TINUR- NGFI
AX345415 Sequence
BC066890 Homo sapi
S77154 Danio rer
BC066890 Homo sapi
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Submitted (30-NOV-1995) Naganari Ohkura, National Cancer Center
Submitted (30-NOV-1995) Naganari Ohkura, National Cancer Center
Research Institute, Growth Factor Division; 5-1-1 Tsukiji, Chuo-ku,
Tokyo 104-0045, Japan (B-mail:nohkura@gan2.ncc.go.jp,
Tel:81-3-3542-2511(ex.4302), Fax:81-3-3542-8170)
Location(Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukamalia; Etheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 3802)
Ohkura,N., Ito,M., Tsukada,T., Sasaki,K., Yamaguchi,K. and Miki,K. Structure, mapping and expression of a human NOR-1 gene, the third member of the Nur7/NGFI-B family
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Homo sapiens NOR-1 mRNA for neuron derived orphan receptor,
complete cds.
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/db_xref="taxon:9606"
/chromosome="9"
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AX067954
AX827766
RRU01146
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RATRNR1X
BC066890
S77154
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AC142180
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BCC09288
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BC076176
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/dev_stage="fetus"
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/gene="NOR-1"
/codon_start=1
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CQ722907 Sequence
AJ011768 Sus scrof
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           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Ockura,N., Ito,M. and Miki,K.
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                                                                                                                      OS Homo sapiens (human)

PN JP 1997084585-A/1

PD 31-MAR-1997

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linear PAT rrtebrata; Bute Hominidae; Hom	AUTHORS Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horrigan, S., Soppet, D.R. and Weaver, Z. TITLE Cancer gene determination and therapeutic screening using signature gene sets JOURNAL Patent: WO 0194629-A 229 13-DEC-2001; Avalon Pharmaceuticals (US) FEATURES Location/Qualifiers source 14977 /organism="Homo sapiens" //mol trype="unassigned DNA" //www.coc.et/	IGIN Query Match 75.8*; Score 2875; DB 6; Length 4977; Best Local Similarity 98.1%; Pred. No. 0; Matches 3008; Conservative 0; Mismatches 40; Indels 19; 733 CCCTGCGTCCAAGCCCAATATAGCCCTTCCCCTCCAGGTTCCAGTTATGCGG	Db 94 CCTGTCGTCCAAGCCCAATATAGCCCTTCCCCTCCAGGTTATGCGGTCGTCAGA 153	911 TCGTGGAGGCTACTCGAGCAACTACGAACTCCAAGCCTTCCTGCGTGTACCAAATGCAGC	QY 1031 ACCACCACCACCACCACCACCAGCAGCATCAGCATCCTTCCT	Qy 1151 CCACCCCACCACCACGCCGCAGGCGGGGGGCGTTATGGGACGAGGCACTGC 1210 bb 514 CCACCCCACCACCACCACCACCCGCAGGCGGGGGGGTTATGGGACGAGGCACTGC 573 Qy 1211 CCTCGGCGCCCGGCTGCTGCCGCGGCGGCGCGCGCGCGC	ATCCCC ATCCCC ATCCCC CCCCC CCCCCC

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1631 GCCAGCACTACGGCGTGCGAACCTGCGAGGGCTGCAAGGGCTTTTTCAAGAGAACAGTGC 1 994 GCCAGCACTACGGCGTGCGAACCTGCGAGGGCTGCTATTTCAAGAGAACAGTGC 1 1691 AGAAAAATGCAAAATTGCTTGCCTGCGAATAAAAAACTGCCCAGTAGACAGAGACGTC 1 1054 AGAAAAATGCAAAATTGCTTGCCTGGCAAATAAAAACTGCCCAGTAGACAAGAGACGTC 1 1751 GAAACGATGTCAGTACTTTGCCTGGCAAATAAAAACTGCCCAGTAGACAAGAGAAG 1 1751 GAAACGATGTCAGTACTGTCGATTTCAGAAGTGTCTCAGTGTTAGGTAAAAGAAG 1 1114 GAAACCGATGTCAGTACTGTCGATTTCAGAAGTGTCTCAGTGTTAGGAAAGAAG 1 1114 GAAACCGATGTCAGTTTCAGAAGTGTCTCAGTGTTAGAATGGTAAAAGAAG 1	Oy 1811 TIGTCCGTACAGATAGTCTGAAAGGGAGGAGGTCTGCCTTCCAAACCAAAGAGC 1870	1354 CCACTGACCAGGCTGCTGCAGGCACAGATGCTGAGCACAATTCTACAACCTCC 14 2051 TGACAGCCTCCATTGATGTATCCAGAAGCTGGGCAGAAATTCCGGGATTTACTGATC 14 1414 TGACAGCCTCCATTGATGTATCCAGAAGCTGGGCAGAAAAGATTCCGGGATTTACTGATC 14 2111 TCCCCAAAGAAGATCAGACATTACTTATTGAATCAGCCTTTTTTGGAGCTGTTTGTCCTCA 21 1474 TCCCCAAAGAAGATCAGACATTACTTATTGAATCAGCCTTTTTTGGAGCTGTTTGTCCTCA 21 1474 TCCCCAAAGAAGATCAGACATTACTTATTGAATCAGCCTTTTTTGGAGCTGTTTGTCCTCA 15	Qy 2171 GACTTTCCATCAGGTCAAACACTGCTGAAGATAAGTTTGTGTTCTGCAATGGACTTGTCC 2230 IS34 GACTTTCCATCAGGTCAAACACTGCAAAGATTTGTTCTTCTGCAATGGACTTGTCC 1593 Qy 2231 TGCATCGACTTCAGTGGCTTTGGGGAGTGGCTCTGTTTAAAGACTTTT 2290 Db 1594 TGCATCGACTTCAGTGCTTCGTGGATTTGGGGAGTGGCTCTGTTAAAAGACTTTT 1690 Qy 2291 CCTTAAAATTTGCAGAGCCTGGAATTTGGGGAGTGGCTTGATTAAAGACTTTT 1653 Db 1654 CCTTAAAATTTGCAGAGCCTGAACCTTGATTATCCAAGCCTTGACTGCTGTCAGCACTTTT 1653 Db 1654 CCTTAAAATTTGCAGAGCCTGAACCTTGATTATCCAAGCCTTAAGCCTTGTTTTT 1330 1654 CCTTAAAATTTGCAGAGCCTGAACCTTGATATCCAAGCCTTAAGCCTTGATCAGCACTGA 1713	Qy 2351 GCATGATCACAGAAAGACATGGGTTAAAAGAACCAAAGAGTCGAAGAGTCTGAACACA 2410 Db 1714 GCATGATCACAGAAAGACATGGGTTAAAAGAACCAAAGAGACTCGAAGAGTTAGCAACA 1773 Qy 2411 AGATCACAAGCAGTTAAAAGACCACCAGAGTAGGACTCTGGAGCCCACCGAGT 2470 Db 1774 AGATCACAAGCAGTTTAAAAGACCACCAGAGTAAGGGACACCTCTGAGCCCACCGAGT 1833 Qy 2471 CCAAAGCAGTTTAAAAAAACCCACAAGAGAAAGAGACTCTGAAGCCCTCCAGCGCA 2530 Qy 2471 CCAAAGCTCTGGGGGCCTCGTGTAAAAAAACTGAGGAACTCTGAGGCCTCCAGCGCA 2530 Db 1834 CCAAGGTCCTGGTAGAACTGAGGAAACTTGCACCCTGGGCCTCCAGCGCA 2530 1834 CCAAGGTCCTGGGTAGAACTGAGGAAACTTGCACCCTGGGCCTCCAGCGCA 1893	Oy 2531 TCTTCTACCTGAAGCTGGAAGACTTGGTCTCCACCTTCCATGACAAGCTCTTCC 2590 1894 TCTTCTACCTGAAGCTGGAAGACTTGGTGTCTCCACCTTCCATCATTGACAAGCTCTTCC 1953 Qy 2591 TGGACACCCTTCTAATCAGGAGCAGTGGAGCAGTGGCTCCTCCTTCCT
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1759 ATTACANGGGANCTTTCTCAGCCTCTCCCACCTTCTCTCCACATCTGATGATCGATC	RESULT 6 S81243 S81243 S81243 S81243 S81243 DGFINITION CHN=steroid/thyroid orphan receptor homolog gene [human, fetal brain, mRNA Partial, 2714 nt]. ACCESSION S81243 VERSION S81243.1 GI:1311504 KEYWORDS SOURCE GORGANISM Homo sapiens (human)
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AGCCTCCGCTGGAGAGACCCCCAGCCCCACTTCAGCGCGCAAGATACCCTCCAGATAT
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/gene="CHN"
/note="steroid/thyroid orphan receptor homolog gene; rat
NOR1 homolog"
       Craniata, Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                443. .2497
/gene=ECRN"
/note="steroid/thyroid orphan receptor homolog gene; No start codon was found. N-terminal of protein truncated kernomosomal breakpoint 2 nucleotides 5' of first (Pro) codon"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 2714)

Clark,J., Benjamin,H., Gill,S., Sidhar,S., Goodwin,G., Crew,J., Gusterson,B.A., Shipley,J. and Cooper,C.S.
Fusion of the EWS gene to CHN, a member of the steroid/thyroid receptor gene superfamily, in a human myxoid chondrosarcoma of152889

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entry (NCBI gibbsq 176289) from the original journal article.
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Db 2539 CTGCTTGCTACGAAGGGATAGGTTTGGAAACCTATCATTTCCTGTCCTTCCT	### ##################################	SOURCE RATTUB NOTVEGICUS (NOTWAY FAL) ORGANISM RATTUB NOTVEGICUS ELEATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. REFERENCE 1 (bases 1 to 4400) AUTHORS OOKUTA,N., Hijikuro,M., Miki,K. and Yamamoto,A. TITLE NUCLEUS RECEPTOR FORMED IN APOTOSIS OF CEREBRAL NEUROCYTE AND	NUCLEUS RECEPTOR GENE CODING THE RECEPTOR JOURNAL PATENT ORP TERUMO CORP COMMENT OS Rattus norvegicus (rat) PN 1996023980-A/1 PD 30-JAN-1996	CONCRA NAME TO TO TO THE TOTAL TO THE TOTAL TO THE TOTAL TOT		FT source 14400 FT /organism='Rattus norvegicus' FT /tissue_type='brain'	sc_RNA 1576183	rce	ORIGIN Query Match 65.9%; Score 2500; DB 6; Length 4400;	14 8 ; CCCGG	Db 1 CGAGTCCTGCCTCCCGCCCCCCCGGCGCTCTTTTTTTTTT	Db 61 ACACAGACACGCTCACACCCGCTCACTTGCACACACAGACACGGGGGTCACAC 120 0v 166 GCTCGGAACACACACACTC-TCGCTCTCGGGGGGGGTCACCCCTTGCCCTGAGCCCTT 223	
	1752 AAACCGATGTCAGTACTGTCGATTTCAGAAGTGTCTCAGTGTTGAAATGGTAAAAGAAGT 1811	1872 ATTACAACAGGAACCTTCTCAGCCCTCTCCACCTTCTCCCATCTGCATGATGAATGC 1931	CACTGACCAGGCTGCTGCAGGCACAGATGCTGAGCATGTGCAACAATTCTACAACCTCCT CACTGACCAGGCTGCTGCAGCACAGATGCTGAGCATGTGCAACAATTCTACAACCTCCT CACTGACCAGGCTGCTGCAGGCAGAGATGCTGCAACAATTCTACAACCTCCT GACAGCCTCCATTGATGTATCCAGAAGCTGGGCAAAAAAATTCCGGAATTACTGATCT IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	2112 CCCCAAAGAAGATCAGAATACTAATTGAATCAGCCTTTTTGGAGCTGTTGTCCTCAG 2171	2172 ACTITICCATCAGGTCAAACACTGCTGAAGATAAGTTTGTGTTCTGCAATGGACTTGTCCT 2231	2232 GCATCGACTTCAGTGCCTTCGTGGATTTGGGGAGTGGCTCGACTCTATTAAAGACTTTTC 2291 	2292 CTTAAATTIGCAGAGCCTGAACCTIGATAICCAAGCCTTAGCCTGCCTGTCAGCACTGAG 2351 	2352 CATGATCACAGAAAGACATGGGTTAAAAGAACCAAAGAGGTCGAAGAGCTATGCAACAA 2411 	2412 GATCACAAGCAGTTTAAAAGACCACAGAGTAAGGGACAGGCTCTGGAGCCCACCGAGTC 2471 	2472 CAAGGTCCTGGGTGCCCTGGTAGAACTGAGGAAGATCTGCACCCTGGGCCTCCAGCGCAT 2531 	2532 CTTCTACCTGAAGGCTGGAAGACTTGGTCTCCACCTTCCATCATTGACAAGCTCTTCCT 2591 [2592 GGACACCCTACCTTTCTAATCAGGAGCAGTGGAGCAGTGAGCTGCCTCCTCTCCTAGCAC 2651	CTGCTTGCTACGCAGCAAAGGGATAGGTTTGGAAACCTATCATTTCCTGTCCTTCCT

1254 GGCGCGCCGCCCCGCGCCCCCCGCCCCCCCCCCCCC	2238 ACTTCAGTGCCTTCGTGGATTTGGGGACTCGACTCTATTAAAGACTTTTCCTTAAA 2297 [
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234 GCCGGTGCAGCGCGCGCCCCAACCCCCCCCCCGGGCTCACTTTGCAACG 2.0 139 GCCGGT-CGCAGCGCGCGCCCCCACCCCCCCCCCCC	CACCACGCCGCCCCCCCCCCCCCCCCCCCCCCCCCCCC

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Qy 3464 GATTACATGTATTTGGTTGTGT-TCTATCACCCCACCAGAGTTCCCTAAACTTG 3522 Db 3471 [A	RESULT 8 AX587468 LOCUS DOUGHS DEFINITION Sequence 3 from Patent WO0246391. ACCESSION AX587468.1 GI:27656292 SEWONDS SOURCE ORGANISM Rattus norvegicus Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Rattus. Rattus. Rattus. Rattus. Rattus. Rattus. Rattus. Rattus. Rattus. Rattus. Rattus. Rattus. Rattus. Rattus.	REFERENCE 1 AUTHORS Guenther, C. and Allen, K.D. AUTHORS Guenther, C. and Allen, K.D. TILE JOURNAL Patent: WO 0246391-A 3 13-JUN-2002, Deltagen, Inc. (US) FATURES Location/Qualifiers 1. 4400 /organism="Rattus norvegicus" /mol_type="unassigned DNA" ORIGIN	Query Match 65.9%; Score 2500; DB 6; Length 4400; Best Local Similarity 83.4%; Pred. No. 0; No. 0; Matches 3131; Conservative 0; Mismatches 535; Indels 90; Gaps 22; Qy 46 CGGAGTCTCCTGCCTCCCGCCCCCACCCCTACCTCCTGCTCCTCCGCTCCCCTT 105 Db 1 CCGAGTCTCCTGCTCCCGCCCCCCATCCAGGCCTGCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCCTCC	Qy 106 ACACAGACGCGCTCACACCCGCTCCTCACTCGCACACACA	224 GCCGGTGCAGCGCGCGCGCACGCCCCTCCCGGGCTCACTTTGCAACG 27	Oy 279 CTGACGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
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1458 CGGGCTGCCCAAGAGGCGGCCCCGCTGGCCTTCCGGCCTCGGCCTCACGCC 1517	1638 CTACGGCGTGCGAACCTGCGAGGCTTTTTCAAGAGAACAGTGCAGAAAA	1758 ATGTCAGTACTGTCGATTTCAGAAGTGTCTCAGTGTTGGAATGGTAAAGAAGTTGTCCG 1817	1878 ACAGGAACCTTCTCAGCCCTCTCCACTCTCCAATCTGCATGATGAATGCCCTTGT 1937	1998 CCAGGCTGCTGCAGGCACAGATGCTGACCACTACTACAACTTCTACACCTCCTGACAGC 2057	2118 AGAAGATCAGACATTACTTATTGAATCAGCCTTTTTTGGAGCTGTTTGTCTCAGACTTTC 2177 2094 AGAAGATCAGACGTTACTATAGAATCAGCCTTTTTTGGAGCTGTTCTTAGACTTTC 2153 2178 CATCAGGTCAAACATGAGATAAGTTTTGTGTTCTGCAATGGACTTGTTCTTAGACTTTC 2137 2154 TATCAGGTCAAAACATGAAGATAAGTTTGTGTTCTGCAATGGACTTGTCTCTGCATGGACTTGTCTCTGCAATGGACTTGTCTCTGCAATGGACTTGTCTCTGCAAAGACTGACT	2238 ACTTCAGTGCCTTCGTGGATTTGGGGAGTGGCTCGACTCTATTAAAGACTTTTCCTTAAA 2297 [CACAGAAAGACATGGGTTAAAAGAACCAAAGAGAGTCGAAGAGCTATGCAACAAGATCAC 241 CACAGAAAGACATGGGTTAAAAGAAACCAAAGAGAGTCGAAGAGCTATGCAACAAGATCAC 241 CACAGAGCGACATGGGTTAAAAAGAAACCAAAGAGAGTGGAGGGGGTATGCAACAAGATCAC 239 AAGCAGTTTAAAAAGACCACAGAGTAAGGGACAGGTCTGGAGGCCCACCAAGGT 247	2478 CCTGGGTGCCTGGTAGAACTGAGGAACTCTGGAGCCTCTGGAGCCCTCAGAGCCCAAGCT 2453 2478 CCTGGGTGCCTGGTAGAACTGAGGAAGATCTGCACCCTGGGCCTCCAGCGCATCTTCTA 2537 11
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                                                                                                                VILL-MGC Project URL: http://mgc.nci.nih.gov
Conteat: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James Lin, University of Iowa
Tissue Procurement: Dr. James Lin, University of Iowa
Tissue Procurement: Dr. James Lin, University of Iowa
CDNA Library Preparation: M. Bento Soares, University of
DNA Sequencing by: The I.M.A.G.E. Consortium (LIML)
Thomas L. Casavant.
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Conteat: bento-soares@wilowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A., Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K., Schaefer,K., Schaefer,K., Schaefer,K., Casavant,T., Soares,M.B.
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7657396.
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Direct Submission
Submitted (25-MAR-2004) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
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0; Mismatches 553; Indels
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/mol type="mRNA"
/stain="C57BL/6"
/db xref="taxon:10090"
/clone="IMAGE:30534822"
/tissue type="Mrain"
/clone_Tib="NIH_BMAP_GIO"
/lab host="DHIDB"
/note="Vector: pYX-ASC"
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Best Local Similarity 82.9%;
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61 GCTGGAGAGCCCCCACCATTCAGCGCGAAGATACCCTCCAGATATGCCCTGC 120 739 GTCCAAGCCCAATATAGCCCTTCCCTCCAGATATGCGGCGCAGACATACAGC 798	919 GGCTACTCGAGCAACTACGAACTTCCTGCGTGTACCAAATGCAG 969	111 111		1468 CCGCCGCCGCGCGCGCGCCGCGCCCCCGCCCCCGIACGGGCTGCCA	TCTGGCGAGGCACGTGTGCGGGGACAACGCCGCCTGCCAGCACTACGCGTG 164
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AJ011767 AJ011767.1 neuron-deriv factor. Sus scrofa Sus scrofa Eukaryota; N Mammalia; E; 1 Cases-Länghc express Unpublished	REFERENCE 2 (bases 1 to 5115) AUTHORS Castello,A. TITLE Direct Submission JOURNAL Submitted (08-OCT-1998) Castello A., Patologia Molecular y JOURNAL Submitted (08-OCT-1998) Castello A., Patologia Molecular y JOURNAL Submitted (08-OCT-1998) Castello A., Patologia Molecular y Terapeutica, Instituto de Investigaciones Biomedicas, C.S.I.C., Jordi Girona, 18-26, Barcelona, 08034, SPAIN Location/Qualifiers Location/Qualifiers Locatio	gene /tissue lib="smooth muscle" /tissue lib="smooth muscle" 1. 5115 /gene="NOR-1" 411 /gene="NOR-1" /gene="NOR-1" /function="transcription factor" /note="alfa transcription factor" /codon start=1 /product="nouron-derived orphan receptor-1 alfa"		3'UTR 20445115 /gene="NOR-1" /notes-alfa transcript" polyA_signal 21682173 /gene="NOR-1" /notes="Affa transcript" /gene="NOR-1" /gene="NOR-1"	ORIGIN Query Match 62.5%; Score 2371; DB 4; Length 5115; Best Local Similarity 87.4%; Pred. No. 0; Matches 2832; Conservative 0; Mismatches 295; Indels 114; Gaps 17; Qy 619 GGCAGCACCAGCCTCGCCGGACGTCCCTCCTCCTACACTTCTAGCTTC 678 1 GGCAGCGCCGCCGCTTCGCCTCGCCGACGCTCCTCCACTTCTAGCTTC 60 Oy 679 GCTGGAGAGACCCCCAGCCCAGCCCACCCAACATAGCCCTGC 738 Qy 679 GCTGGAGAGACCCCCAGCCCCACCCAACACAAAAAGCCTCCTCCACTTCTCAGCTTTC 60

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1768 IGTCGATTTCAGAAGIGTCTCCAGIGTTGGAATGGIAAAAGAAGTTGTCCGTACAGATAGT 1827	CTGAAAGGGAGGAGAGGTGTGTCTGCCTTCCAAACCAAA	TCTCAGCCCTCTCCACCTTCTCCTCCAATCAGATGAATGCCCTTTGTCCGAGCTTTA	ACAGACTCAACCCCAGAGATCTTGATTATTCCAGATACTGTCCCACTGACCAGGCTGCT	GCAGGCACAGATGCTGAGCATGTGCAACAATTCTACAACCTCCTGACAGCCTCCATTGAT	GTATCCAGAAGCTGGGCAGAAAGATTCCGGGATTTACTGATCTCCCCAAAGAAGATCAG 2	2128 ACATTACTTATTGAATCAGCCTTTTTGGAGCTGTTTGTCCTCAGACTTTCCATCAGGTCA 2187	2188 AACACTGCTGAAGATAAGTTTGTGTTCTGCAATGGACTTGTCCTGCATCGACTTCAGTGC 2247	CTTCGTCGATTTGGGGAGTGGCTCGACTCTATTAAAGACTTTCCTTAAATTTGCAGAGC	CTGAACCTTGATATCCAAGCCTTAGCCTGCCTGTCAGCATGAGCATGATCACAGAAAGA	2368 CATGGGTTAAAAGAACCAAAGAGGGTCGAAGAGTTGCAACAAGATCACAAGAGTTTA 2427 	2428 AAAGACCACCAGCAGTAAGGGACAGGCTCTGGAGCCCACCGAGTCCCAGGGTGCC 2487	CTGGTAGAACTGAGGAAGATCTGCACCCTGGGCCTCCAGGGCATCTTCTACCTGAAGCTG	CTTTC 2		CAGCTC	2727 CTGTAGAAAGCAAAGAC	2764 ITTCCTTACAACCTAAAAGCCAGAAAACTTGCAGTATTGTGTTGGGGTTGTGTTTTATA 2823

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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8634690
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Submitted (21-JUL-1995) Y. Labelle, INSTITUT CURIE, SECTION IRCHERCHE, 26 RUE DULM, 75231 PARIS CEDEX 05, FRANCE
Location/Qualifiers
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X89894
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nuclear receptor.
Homo sapiens (human)
Homo sapiens
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Labelle, Y.
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Db 1381 GGCAGCCAGCCGCGCTTGAGAGCCACCCGTACGGGCTGCCGCTGGCCAAGAGGGGG 1440 Qy 1483 GCCCGGTTGGCCTTCCGCCTCTGGGCCTCCCCTACCGGTCCAGCCTGCTG 1542	1543	Qy 1603 TGTGCGTGTGTGCGGGACAACGCCGCCTGCCAGCACTACGGCGTGCGAACCTGCGAAGGC 1662 Db 1561 TGTGCCGTGTGCGGAACAACGCCCCTGCCAGCACTACGGCGTGCGAACCTGCGAAGGC 1620	TGCAAGGCTTTTTCAAGAGAACAGTGCAGAAAATGGCAAAAATATGTTTGCCTGGCAAATTTTTTGCCTGGCAAATTTTTTGCTGGCAAATATGCAAAATATGCAAAATATGCTTTTGCCTGGCAAATTTTGCTGGCAAAATATGCAAAATATGCAAAATATGCTTTTGCCTGGCAAAA	AAAAACTGCCCAGTAGACAAGAGGCGTGGAAACCGATGTCAGTACTGTCGATTTCAGAAG 	1783 TGTCTCAGTGTTGGAAAAGAAGTTGTCCGTACAGATAGTCTGAAAGGAGAGAGA		CACCC CACCC		SULT 13	LOCUS LOCUS AX587466 1884 bp DNA linear PAT 10-JAN-2003 ACCESSION AX587466 AX587466 AX587466 AX587466 AX587466 AX587466	S Mus musculus (house mouse) ISM Mus musculus (house mouse) Five moust mouse mouse mouse)	irogna	Tansyen Patent: V Deltagen,	control cont	<pre>y Match 19.2%; Score 1485.6; DB 6; Length 1884; Local Similarity 87.2%; Pred. No. 1.1e-231; hee 1643. Concerning # 10.0 Minmatch 2010; 1.1e-2</pre>		790 ACATACAGTTGGAATACACCAGGAGATCATGAACCCCGACTACACCAGGTGACCATG

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/gene="Tec"
/note="similar to NOR-1, MINOR, CHN"
           1. .1884
/organism="Mus musculus"
/mol type="mRNA"
/db_xref="taxon:10090"
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Sciurognathi; Muridae; Murinae; Mus.
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Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostom
Bukaryota; Merazoa; Chordata; Sciurognathi; Muridae; Murinae; M
1 (bases 1 to 1884)
Maltais, A and Labelle, Y.
Structure and expression of the mouse gene encoding the orphan
nuclear receptor TEC
DNA Cell Biol. 19 (2), 121-130 (2000)
                                                                                                                                                                                                                                                                                                                                                     CTCAGACTITCCATCAGGTCAAACACTGCTGAAGATAAGTITGTGTTCTGCAATGGACTT
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AATGCCCTTGTCCGAGCTTTAACAGACTCAACACCCAGAGATCTTGATTATTCCAGATAC
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Direct Submitted (30-58P-1999) Research Center, Pavillon St-Francois d'Assise, 10, rue de l'Espinay, Quebec, Qc GlL 3L5, Canada
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1681 ACCAAGATCACAAGCAGCTTAAAGGACCACCAGAGGAAGGA	AL1358937 AL1358937 AL1358937 AL1358937 AL1358937.16 GI:16973850 AL1358937.16 GI:16973850 AL1358937.16 GI:16973850 AL1358937.16 GI:16973850 HOMO sapiens (human) AL1 (bases 1 to 146889) BENKATYORA, ME THER Sampe Catarrhini; HOMO SADDINITE (Ich NOV-2001) Wellcome Trust Sampe Cambridgeshire, CB10 15A, UK. B-mail enquiring humquery@sanger.ac.uk Clone requests: cloner on Nov 17, 2001 this sequence version replaced the where differences are found these are amnota together with a note of the overlapping clone, as wonly a small overlap as described above. This sequence was finished as follows unless regions were either double-stranded or seque chemistry or covered by high quality data (is 30); an attempt was made to resolve all sequence subclains succeed the passing subclone or more than one M13 suassembly was confirmed by restriction digest abbreviations are used to associate primary in the feature table with their source datab SNISSROT; Tr. TRENSE; WP:, WORMPEP; Inform database can be found at http://www.sanger.ac.uk/RGP/Chr.9 RP11-6013 is from the library RPCI-11.1 cons Platet of Tom part of Lone Chromosome 9, constructed by the Sanger Cent Grow Further information can be found at http://www.sanger.ac.uk/RGP/Chr.9 RP11-6013 is from the library RPCI-11.1 cons Platet of Group. Further information can be found at http://www.chori.org/bacpac/home.htm VECTOR: pBACc3.6 IMPORTANY: This sequence is not the entire in RP11-6013 it may be shorter because we sequence that the right end of clone RP11-16 folia the true right end of clone RP11-16 folia the true right end of clone RP11-16 folia the received the right end of clone RP11-16 folia the received the right end of clone o	Ä
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anger Institute, Hinxton, inries:
onerequest@sanger.ac.uk
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ntre Chromosome 9 Mapping
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Hominidae; Homo.
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Db 26455 TATC Oy 3380 CAAC Oy 3440 GAAU Oy 3500 CCC Oy 3500 CCC Oy 350 AGCC Oy 360 AGCC Oy	Search completed: Job time : 15982 8
Clone="RPI1-6013"	2720 GCAGCTCCTGTAGAAAGCAAAGACTTTTTTTTTTTTCTGGCTCTTTTCTTACAACCTAA 2779 2885 GCAGCTCCTGTAGAAAGCAAAGCTTTTTTTTTTTTTTTT

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Adg56733 CDNA sequ
Adb15573 DNA encod
Adb84033 Human NUR
Adb84033 Human CDN
Add2804 Human CDN
Adg23739 PRO polyp
Adb84053 Rat WURR1
Aac67273 Human CDN
Adb84058 Human nuc
Adb84058 Murine NU
Adb84032 Murine NU
Adb84038 Murine NU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to a novel method for examining allergic diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Examining allergic diseases e.g. atopic dermatitis by differential display based on gene expression of NOR-1 receptor protein, also applicable in screening compounds for treatment of allergic diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  human, gene, 88; allergic disease, NOR-1; MINOR; eosinophil; atopic dermatitis, antiallergic; antiinflammatory; dermatological.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Saito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yayoi Y, Sugita Y,
                                                                                                                                                                                                                                                                                                                                                                                                                            Human NOR-1 (MINOR) cDNA sequence SegID 1.
                                                                                                                                                                                                                                                                                                       ALIGNMENTS
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/product= "NOR-1 protein"
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                       ADB84081
ADB84081
AAQ56733
AAQ56733
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ADH28985
ACC821074
ADH37169
ADB25697
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ADB4053
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ADB84058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
730. .2610
/*tag= a
                                                                                                                                                                                                                                                                                                                                                             ADI13007 standard; cDNA; 3794 BP
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(NIGE-) JAPAN GEN AGENCY NATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-JUN-2003; 2003WO-JP008199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JUN-2002; 2002JP-00188490
   Hashida R, Kagaya S,
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P-PSDB; ADI13008.
   WO2004003198-A1
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     Adi13007 Human NOR
Abk51689 Human nuc
Abk81698 Human nuc
Adi57170 Human NOV
Ade25701 Human cDN
Abx62937 Human act
Abx62937 Human neu
Adf2886 Human nor
Abl61892 Colon ade
Abk84229 Human CDN
Adi14062 Human PRO
Adi14062 Human NF-
Adi31602 Human NF-
Adi31602 Human CDN
Adi31602 Human cDN
Adi28873 Pig nor-1
Adf28873 Pig nor-1
Adf28873 Pig nor-1
Adp85436 Murine Ne
Adf28871 Pig nor-1
                                                                             March 21, 2005, 04:05:50 ; Search time 1901 Seconds (without alignments) 11814.571 Million cell updates/sec
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                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                          - nucleic search, using sw model
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that comprises comparing the expression levels of a gene encoding the NOR 1 receptor protein between patients and healthy individuals. Specifically, the NOR-1 gene, also referred to as MINOR, is expressed in the specialist white blood cells known as escinophils and is involved in mediating an allergic reaction. The present invention describes a differential display method that can identify the expression level of this gene in order to identify its usefulness in diagnosing allergic diseases such as atopic dermatities. Purthermore, compositions can also be used to screen compounds for the treatment of allergic diseases. Accordingly, they exhibit various activities including antiallergic, antiinflammatory and dermatological. This polynucleotide sequence is the human NOR-1 cDNA sequence of the invention. 0

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	841	CTGACCATGGACCTTGGCAGCACTGAGATCACGGCTACAGCCACCACGTCCCTGCCCAGC 900
	901	ATCAGTACCTTCGTGGAGGGTACTCGAGCAACTACGAACTCAAGCCTTCCTGCGTGTAC 960
	961	CAAATGCAGCGGCCCTTGATCAAAGTGGAGGGGGGGGGG
	1021	
	1081	
	1141	
	1201	
	1261	
	1321	CCGCATCCCCCCGCGCCCAGCCCGCCGCCACCACCTCGGCTACGACCGAC
	1381	
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	1621	AACGCCGCCTGCCAGCACTACGGCGTGCGAACCTGCGAGGGCTGCAAGGGCTTTTTCAAG 1680
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	1741	AAGAGACGTCGAAACCGATGTCAGTACTGTCGATTTCAGAAGTGTCTCAGTGTTGGAATG 1800
	1801	GTAAAAGAAGTIGICCGTACAGATAGICIGAAAGGGAGGAGAGAGGTCGTCTGCCTTCCAAA 1860
	1861	861 CCAAAGAGCCCATTACAACAGGAACCTTCTCAGCCCTCTCCACCTTCTCCTCCAATCTGC 1920

Oy 3001 ACAGCCAAGGGTTGTTCGCCAGGGTAGGATTGTCTTAAAGATTGGTCCCTTGAAAATAT 3060 1001 ACAGCCAAGGGTTGTTCGCCAGGGTAGGATCTCTTAAAGATTGGTCCCTTGAAAATAT 3060 3001 ACAGCCAAGGGTTGTTCGCCAGGGTAGGATCTGTTTAAAGATTGGTCCCTTTAAATTT 3060 Oy 3061 GCTTCCTGTATCAAAGGTACGTATGTGGTGCAAACAAGGCAGAAACTTCCTTTTAATTTC 3120 Oy 3121 CTTCTTCCTTTATTTTAACAAATGGTGAAAGAGCAGAAACTTCCTTTAATTTC 3120 Oy 3121 CTTCTTCCTTTATTTTAACAAATGGTGAAAGAGTGCAGAATTACCTACAAATCAGACATGG 3180 OY 3181 CAAAACAATAATGGTGAAAAGAGTGCAAAACAAATCAAATCAGACATGG 3180 OY 3181 CAAAACAATAATGGTTTGCTTCCATAAACAAGTGCTATTTTTAAAGTGCTGTCTTA 3240 1181 CAAAACAATAATGGCTGTTTGCTTCCATAAACAAGTGCAATTTTTTAAAGTGCTGTCTTA 3240 3181 CAAAACAATAATGGCTGTTTGCTTCCATAAACAAGTGCAATTTTTTAAAGTGCTGTCTTA 3240	Oy 3241 CTAAGTCTTGTTTATTAACTCTCTTTATTCTATATGGAAATAAAAAGGAGCCAGTCATG 3300 3241 CTAAGTCTTGTTTATTAACTCTCTTTATTCTATATGGAAATAAAAAGGAGCAGTCATG 3300 Qy 3301 TTAGCAAATGACGTTAATATCCTTAGCAGGCTGTTCACCTTCCCTGTCGATCCC 3360 Db 3301 TTAGCAAATGACGTTAATATCCCTAGCAGAGGCTGTTCACCTTCCCTGTCGATCCC 3360 Qy 3361 TTCTGAGGTATGGCCATCAAAGGAGGCTGTTCTTCTGATGGAACCAGATCCCTGC 3420 Db 3361 TTCTGAGGTATGGCCCATCTAAAAACGAGCATTCTTGATGGAACCAGATCCTTGCTGC 3420 TTCTGAGGTATGGCCCATCCAAGACTTTTAGGCCATTCTTGATGGAACCAGATCCTTGCTGC 3420	Qy 3421 CTGACTGTCCAGCTATCCTGAAAGTGGATCAGATTATAAACTGGATTACATGTAACTGTT 3480 Db 3421 CTGACTGTCCAGCTATCCTGAAAGTGGATCAGATTATAAACTGGATTACATGTAACTGTT 3480 Qy 3481 TTGGTTGTTCTATCAACCCCACCAGAGTTCCCTAAACTTGCTTCAGTTATAGTAACTG 3540 Db 3481 TTGGTTGTTCTATCAACCCCACCAGAGTTCCCTAAACTTGCTTCAGTTATAGTAACTG 3540 Qy 3541 ACTGGTTGTTCTATCATCAGAAGGCCCATAAGTCAGTTAGATCCCTAGATAAGAA 360 Db 3541 ACTGGTATATCAATCAAAGCCCATAAGTCAGTTTTGATCCCTAGATAAGAA 360	QY 3601 CATGCAAATCAGCAGGAACTGGTCATACAGGGTAAGCACCAGGGACAATAAGGATTTTTA 3660 bb 3601 CATGCAAATCAGCAGGACTAACAGGGTAAGCACCAGGACAATAAGGATTTTTA 3660 CY 3661 TAGATATAATTTTTGTTATTGGTTAAGGAGACAATTTGGAGAGCAATCT 3720 Db 3661 TAGATATAATTTTTTTTTTTTTTTTTTTTTTTTTTTTT	3721 TTTTAAAAATAGTATGAATGCTGAATACTAGAAAGATTTAAAAAATAGTATGAGTGTGA 3781 GTACTAGGAAGGAT 3794 3781 GTACTAGGAAGGAT 3794	RESULT 2 ABK51689 standard; DNA; 3802 BP. XX AC ABK51689; XX AC ABK51689; XX
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1921 ATGATGAGTCTTGACGAGCTTGACGACCCAGAGATCTTGATTATTCC 1980	TTGFCCTCAGACTTTCCATCAGGTCAAGATAAGTTTGFGTTCTGCAAT 222	AAAGACTITTCCTTAAATTTGCAGAGCCTGAACCTTGATATCCAAGCCTTAGCCT TCAGCACTGAGCATGAACAAGCATAAAAGAACAAAGAGCTT TCAGCACTGAGCATGAAAGACATGGTTAAAAGAACCAAAGAGAGTCG TCAGCACTGAGCATGATTAAAAGACATGAGTTAAAAGACACAAGAGAGTCG TATGCAACAAGATCACAAGCAGTTTAAAAGACCACCAGAGTAAGAGACCGCTC TTTGCAACAAGATCACAAGCTTTAAAAGACCACCAGAGTAAAGAGACCGCCCAGAGTAAAGAGCCCCCAGAGATCACAAGAGCCCCCAGAGTTAAAAAGACCACCAGAGATAAAGAGACCCCCAGAGATCAAAGAGCCCCCCAGAGAAGATCTGAAGACCCCCCAGAGATCTGAACACCCCCCAGAGATCTGAACACCCCCAGAGATCTGAACACCCCCAGAGATCTGAACACCCCCAGAGATCTGAACACCCCCAGAACATCTAAAAAAAA	CCCACCAGAGTCCAGGGTGCCTGGGTAGAACTGAGGAAGATCTGCACCCTGGGC 252 CTCCAGGGCATCTTCTACCTGAAGCTGGAAGACTGGGTGTCTCCACCTTCCATCATTGAC 258 [TCTCCTAGCACCTGCTTGCTAGCAAGGGATAGGTTTGGAAACCTATCTTGGGTTTCCTG	1

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                  Treating inflammatory immune disease such as arthritis, comprises suppressing expression level of NURR subfamily of nuclear transcription factors, or corticotropin releasing hormone receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                       member. The present nucleic acid sequence represents the human nuclear receptor NOR1 gene of the invention. Note: The present sequence is not shown in the specification but was obtained from Genbank (1651190)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3802 BP; 919 A; 1141 C; 912 G; 830 T; 0 U; 0 Other;
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                                                                                                   BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                Claim 10; Page; 123pp; English.
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                             CTCACCGCCTCCGGGAGCCGCTGGGCTTGTACACCGCAGCCCTTCCGGGACAGCAGCTGT
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The invention relates to detecting (M1) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of G is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the expression of at least one gene in Gs; (2) screening (M3) for an agent capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease using the gene expression or profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from Gs, where the level of expression of the gene is indicative of inflammation; (4) treating (M5) an inflammation (especially chronic) or in a tissue, an allergic response in a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an expression of gene(s) from Gs in the tissue. M1 is useful for detecting GCA; M2 is useful for modulating GA; M3 is useful
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3661 TATAGATATAATTTTTTGGTAATTGGGTTAAGGAGACCAATTTTGGAGGCAAGCA 3720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.
                                                                                        3721 AATCTTCTTTTAAAAAATAGTATGAATGTGAATACTAGAAAAGATTTAAGAAATAGTAT
                                                                  Human; ss, granulocytic cell; DNA chip; bacterial infection; viral infection; parasitic infection; protozoal infection; fungal infection; sterile inflammatory disease; psoriasis; rheumatoid arthritis; glomerulonephritis; asthma; thromboals; cardiac reperfusion injury; renal reperfusion injury; ARDS; adult respiratory distress syndrome; inflammatory bowel disease; crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                Human cDNA differentially expressed in granulocytic cells #269
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anticonvulsant; osteopathic; antiarthritic; antiinflammatory;

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ds; gene; human; antidiabetic; anorectic; cardiant; hypotensive; antiarteriosclerotic; anorectic; virucide; antibacterial; fungicide; protozoacide; nootropic; neuroprotective; antiparkinsonian;
ADL57170 standard; DNA; 3802 BP
                                                                                                                                                                                                                                Human NOV9i gene SEQ ID NO:115.
                                                                                                                                                        03-JUN-2004
                                                                            ADL57170;
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RESULT 4

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The invention relates to a novel isolated polypeptide (NOVX) comprising a mature form of any of the 37 amino acid sequences fully defined in the comparization of any of the 37 amino acid sequences fully defined in the comparization of participation. A polypeptide of the invention has antidiabetic, ancidate, hypotensive, antiparthisonian, antionnulant, osteopathic, antiarthritic, antiinflammatory, dermatological, antiasthmatic, and antiantlammatory, dermatological, antiasthmatic, and antiantlammatory, dermatological, antiasthmatic, and antiantlammatory, the polypeptides, nucleic acid molecules and antibodies are useful in the manufacture of a medicament for treating a syndrome content of associated with a human disease, preferably a NOVX-associated disorder. The nucleic acid molecules, polypeptides and antibodies are useful for treating, preventing or diagnosing diseases such as metabolic disorders, diabetes, obesity, infectious diseases such as metabolic disorders, disease, parkinson's disease, (viral, bacterial, fungal, contential, independent and protocoal), anorexia, cancer, cardiovascular diseases (hypertension, atherosclerosis), neuvodegenerative disorders, Alzheimer's disease, epilepsy, immune disorders and antibodies content and various dyslipidaemias. The nucleic acids and polypeptides as targets for the identification of small molecules that modulate or inhibit e.g. neurogenesis, call differentiation, call contents, and various dyslipidaemias. The identification of small molecules that modulate or inhibit e.g. neurogenesis, call differentiation, call contents, and various disponesis, wound healing and angiogenesis, in generation of antibodies that bind immunospecifically to Novy ansate and antibodies that bind immunospecifically to Novy and antibodies in propertion and antibodies that bind immunospecifically to Novy and antibodies in propertion of antibodies in propertion and antibodies i
                dermatological; antiasthmatic; antilipaemic; gene therapy; fibroblast growth factor receptor 4; FGFR4; complement factor I precursor; matrix matrix metalloproteinase-15 precursor; MDC3; T-lymphocyte autigen Lb-9 precursor; fibroblast growth factor-21; FGF-21; fibroblast growth factor-21; FGF-21; alpha-2 macroglobulin-like polypeptide variant; antileukoproteinase I precursor; LIV-1; nuclear hormone receptor NOR-1; transmembrane protein-like; beta-neoendorphin-dynorphin precursor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated NOVX polypeptides and polynucleotides, useful for preventing, diagnosing or treating NOVX-associated disorders, e.g. osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease, asthma, or infections.
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P-PSDB; ADL57171.
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23-SEP-2002;
23-SEP-2002;
24-SEP-2002;
25-SEP-2002;
30-SEP-2002;
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12-SEP-2002;
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841 1019 839 899 959 1079 1139 1199 1259 1261 1319 1379 1381 1439 1499 1559 1619 1679 1681 1739 1741 1799 1801 1859 1861 781 ద ò . 원 ò ઠ g õ q ઠે 8 ò 셤 ò 요 ઠે 셤 8 ద ઠે 셤 ò 셤 ò q ò g Š ద ઠે 셤 8 셤 ò ద 8 a Proteins: NOV1a-1t show homology to fibroblast growth factor receptor 4 (FGFR4); NOV2a shows homology to complement factor I precursor; NOV3a shows homology to matrix metalloproteinase-15 precursor; NOV4a shows homology to MCG; NOV4a shows homology to Fibroblast growth factor-21 by Percursor; NOV6a-6m show homology to Tibroblast growth factor-21 (FGF-21); NOV7a-7c show homology to global accordant in the polypeptide variant; NOV8a-8g show homology to antileukoproteinase 1 precursor; NOV9a-9 is show homology to LIV-1 protein; NOV1a shows homology to nuclear hormone receptor NOV8-1; NOV11a-11 show homology to beta-neoendorphin transmembrane protein-like; NOV12a-12c show homology to beta-neoendorphin dynorphin precursor. The present sequence encodes a NOVX polypeptide of 120 238 240 178 180 298 358 CGTGGAGGTGGGAACAGCGGGGGATCCTCCCCCTGGTCACAGCCCAAGCCAGGACGCC 360 CGCGGAACCTCTCGGCTGTGCTCTCCCATGAGTCGGGATCGCAGCATCCCCCCACCACCAGCGG 420 480 300 418 478 538 540 598 9 658 9 718 720 778 780 838 9 9 CCGCCCCCCACCCTCCAGCTCCTGCTCCTCCGCTCCCATACACAGACGCGCTCCA CGCCACAGGCACATCAAAGCCCACTGCGGAAGAGGCAGCCCCGGCAAGCCCCGGCAAGCCCCTGAGC GACTCCCCCCCAGTGCAGATTTCGGGACAGCTCTCTAGAAACTCGCTCTAAAAGACGGAAC GACTCCCCCCGGGTGCAGATTTCGGGACAGCTCTCTAGAAACTCGCTCTAAAAGACGGAAC CTCCTACACTCTCAGCCTCCGCTGGAGAGACCCCCAGCCCCACCATTCAGCGCGCAAGAT ATANATGACGTGCCGAGAGAGCGAACGCGCCGGCAGCCGGAGAGCGCAGTCTCCTGCCT ACTICGCICICCCCCCCCCCCCCCCTTGCCCCTGAGCCCTTGCCGGTGCAGCGCGG CGCCGCAGCTGGACGCCCCTCCCGGGCTCACTTTGCAACGCTGACGTGCCGGCAGTGGC GGCCACAGCACTCAAAGCCCACTGCGGAAGAGGCCCGGCCAGGCAGCCCGGGCCCTGAGC CTGGACCCTTAGCGGTGCCGGGCACTGCCGGCGCTTCGCCTCGCCGGACGTCCGCTC CTGGACCCTTAGCGGTGCCGGGCACTGCCGGCGCTTCGCCTCGCCGGACGTCCGCTC CTCCTACACTCTCAGCCTCCGCTGGAGAGACCCCCCAGCCCCACCATTCAGCGCGCAAGAT ATGCGGCGCAGACATACAGCTCGGAATACACCACGGAGATCATGAACCCCGACTACACCA CGCCGCAGCTGGACGCCCCTCCCGGGCTCACTTTGCAACGCTGACGGTGCCGGCAGTGGC CGTGGAGGTGGGAACAGCGGCGATCCTCCCCCCTGGTCACAGCCCAAGCCAGGACGCC ACCTCCAGATATGCCCTGCGTCCAAGCCCAATATAGCCCTTCCCGCTCCAGGTTCCAGTT ACCTCCAGATATGCCCTGCGTCCAAGCCCAATATAGCCCTTCCCCTCCAGGTTCCAGTT Gaps CGCGGAACCTCTCGCTCTCCCATGAGTCGGGATCGCAGCATCCCCCCACCAGCCG CTCACCGCCTCCGGGAGCCGCTGGGGCTTGTACACCGCAGCCCTTCCGGGACAGCAGCTGT 8 Length 3802; Sequence 3802 BP; 919 A; 1141 C; 912 G; 830 T; 0 U; 0 Other; Indels -dynorphin precursor. The present sequence encodes the invention. Ouery Match 98.1%; Score 3722; DB 12; Best Local Similarity 99.4%; Pred. No. 0; Matches 3779; Conservative 0; Mismatches 15; 361 61 61 121 121 179 181 239 241 299 301 359 419 479 539 541 599 601 629 719 779 421 481 721 661 셤 g d ద 셤 q ઠ ઠે ò ઠે ò ઠે ઠે 셤 ठ В δ g ઠે g ò g ò а 셤 õ 8

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299 GAACAGCCAAGGGTGGTCGCCAGGGTGGGTGTTCTTAAAGTTGGTCCCTTGAAAT 3068 3001 GAACAGCCAAGGGTGGTCGCCAGGGTGGTGTGTTCTTAAAGTTGGTCCCTTGAAAT 3060 3005 ATGCTTCCTGTATCAAAGGTACGTGTGTGTGTGCAAACAGCCAAAATTGATTTTAATT 3120 3011 GATGCTCCTTATTTTATTTACAATGGTGAAAACAGCCAAAACTGAATTCAAATCAAACTGAATTTTTAATTTAAAGTGTTGAAAACAAATCAAAATCAAAATCAAAATCAAAATCAAAAAA	RESULT 5 ADE25701 standard; cDNA; 5828 BP. XX AC ADE25701; XX
1919 GCATGATGAMTGCCCTTGTTCCGAGCCTTTAACAGCCTCAACACCCCAGGAATTTTTT 1978 1919 GCATGATGAMTGCCCTTGTTCCGAGCCTTTAACAGCCTCAACACCCCAGGAATTTTTTT 1980 1919 GCATGATGAMTGCCTTGTCCGAGCCTTTAACAGCCTCAACACCCCAGGAATTTTTTT 1980 1919 GCATGATGACTCTCTGACCAGCTTTCAACACCCCAGGAATTTTTTTT	2759 GCTCTTTCCTTACAACCTAAAGCCAGAAAACTTGCAGAGTATTGTGTTGGGGTTGTGT 2818 2761 GCTCTTTTCCTTACAACCTAAAGCCAGAAAACTTGCAGAGTATTGTGTTGGGGTTGTGT 2820 2819 TTATATTTAGGCATTGGGGATGGGGTGGAGGGGTTATAGTTCATGAGGGTTTTCTAA 2878 2821 TTATATTTAGGCATTGGGGATGGGGTGGAGGGGTTATAGTTCATGAGGGTTTTCTAA 2880 2821 TTATATTTAGGCATTGGGGATGGGGTGGAGGGGTTATAGTTCATGAGGGTTTTCTAA 2880 2879 GAAATTGCTAACAAAGCACTTTTGGACAATCCAACCAGGGGAAAAAAAA

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                                                                                                                                                                                                                                                                               The invention relates to a combination comprising several polynucleotides having any one of 127 sequences (S1) such as the sequence of human call calmodulin gene, human mRNA for KIAA0310 protein, leukotriene A4 hydrolase, human CG1-142 protein mRNA, human K+ channel beat 2 subunit mRNA, etc., and their complements. The cDNAs are differentially expressed to him LPS (Hippopolysaccharide)-treated foam cells. Also included are obtaining an extended or full length gene from a library of nucleic acid sequences, an expression vector containing the nucleic acids, a host cell obtaining an extended or full length gene from a library of nucleic acid sequences, an expression vector containing the host cell, and a composition comprising a purified antibody that specifically binds to the proteins. The foam cell-expressed nucleic acids are useful for a high throughput detection of differential expression of one or more composition comparison with a standard defines early, mid or late throughput screening of a library of molecules or compounds to identify a ligand which binds a polynucleotide. The library is chosen for high throughput screening of a library of molecules or compounds to identify a ligand which binds a polynucleotide. The library is chosen from by untifying a ligand from a sample for making a antibody. The compounds to identify at least one ligand which specifically binds a comparison, for purifying a ligand from a sample for making a antibody. The compounds to identify at least one ligand which specifically binds a conforwascular disorder. The foam cell-expressed nucleic acids are useful conformation of a microarray which can be used for detecting related coll-expressed nucleic acids are useful coll-emptre on a microarray which can be used for detecting a category at heavestly diagnosing cardiovascular disease, as elements on a microarray which can be used for detecting a coll-expression is sample, diagnosing cardiovascular disease, is upregulated in LPS treated foam cells.
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                                                                                                                                                                                              Combination containing several polynucleotide that are differentially expressed in foam cells and complements of the polynucleotides, useful for diagnosing cardiovascular disease or atherosclerosis.
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Pred. No. 0;
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                                                                         19-SEP-2001; 2001US-0323784P
                                                                                                       (INCY-) INCYTE GENOMICS INC.
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Best Local Similarity 98.1
Matches 3728; Conservative
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1140 1198 418 420 658 9 720 778 780 840 898 900 958 960 480 600 1119 AGTCCCCACCGTCCACCCCACCACCACCGGGCTTCCCCCCGCAGGCGGGGGGCGTTATGGG CGTGGAGGTGGGAACAGCGGCGGCATCCTCCCCCCTGGTCACAGCCCAAGCCAGGACGCC CGCGGAACCTCTCGGCTGTGCTCTCCCATGAGTCGGGATCGCAGCATCCCCCACCAGCCG 841 AGCTGACCATGGACCTTGGCACCTGAGATCACGGCTACAGCCACCACGTCCCTGCCCA GACTCCCCCCCAGTGCAGATTTCGGGACAGCTCTCTAGAAACTCGCTCTAAAGACGGAAC GACTCCCCCCCAGGGGGGATTTCGGGACAGCTCTCTAGAAACTCGCTCTAAAAGACGGAAC CTGGACCCTTAGCGGTGCCGGGCAGCACTGCCGGCCTTCGCCTCGCCGACGACGTCCGCTC CTCCTACACTCTCAGCCTCCGCTGGAGACCCCCCAGCCCCACCATTCAGCGCGCAAGAT 661 CTCCTACACTCTCAGCCTCCGCTGGAGAGACCCCCAGCCCCACCATTCAGCGCGCAAGAT 721 ACCCTCCAGATATGCCCTGCGTCCAAGCCCAATATAGCCCTTCCCCTCCAGGTTCCAGTT GCATCAGTACCTTCGTGGAGGGCTACTCGAGCAACTACGAACTCAAGCCTTCCTGCGTGT 901 GCATCAGTACCTTCGTGGAGGGCTACTCGAGCTACGAACTCCAAGCCTTCCTGCGTGT 1019 ATCACCACCACCACCACCACCACCACCATCACCAGCAGCAGCAGCATCAGCATCCA 1201 ACGAGGCACTGCCCTCGGCGCCCGGCTGCATCGCACCCGGCCCGCTGCTGGACCCGGCGA CGCGGAACCTCTCGGCTGTGCTCCCATGAGTCGGGATCGCAGCATCCCCACCAGCCG CTCACCGCCTCCGGGAGCCGCTGGGCTTGTACACCGCAGCCCTTCCGGGACAGCAGTGT CGCCACAGACTCAAAGCCCCACTGCGGAAGAGGGCAGCCCGGCAAGCCCGGGCCCTGAGC 541 CGCCACAGCACTCAAAGCCCACTGCGGAAGAGGGCAGCCCGGCAAGCCCGGGCCCTGAGC ATGCGGCGCAGACATACAGCTCGGAATACACCCAGAGATCATGAACCCCGACTACACA AGCTGACCATGGACCTTGGCAGCACTGAGATCACGGCTACAGCCACCACGTCCCTGCCCA TGAAGGCGGTCCCCACGGTGGCCGGCGCGCTTTCCCGCTTTCCACTTCAAGCCCTCGC TGAAGGCGGTCCCCACGGTGGCCGGCGCGCTTTCCGCTTTCCACTTCAAGCCCTCGC CGCCGCATCCCCCCGCGCCCCAGCCCGGCCGGCGCCACCACCTCGGCTACGACCCGACGG ACGAGGCACTGCCCTCGGCGCCCGGCTGCATCGCACCCGGCCCGCTGCTGGACCCGCCGA

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3660
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ACTGACTGGTATATTCATTCAGAAGCGCCATAAGTCAGTTGAGTATTTGATCCCTAGATA 3600
                                                                                                                                                                                                                          T cell; gene; 88; differential expression; T cell activation; antiallergic; cytostatic; immunosuppressive; antimicrobial; gene therapy; allergy; cancer; graft versus host disease; infection; autoimmune disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New combination comprising several cDNAs that are differentially expressed in activated T cells, useful for diagnosing, treating, staging or monitoring treatment for allergy, cancer, infectious and/or autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This invention relates to the sequences of several cDNAs that are differentially expressed in activated T cells. The sequences of the invention may have antiallergic, cytostatic, immunosuppressive and antimicrobial activity and may be used in gene therapy. The invention also comprises a method for screening samples for differentially expressed genes and a method for detecting these cDNAs by hybridisation. The methods and compositions of the present invention are useful for diagnosing, treating, staging or monitoring treatment for allergy; cancer, chronic graft versus host disease, infectious and/or autoimmune disorders. The present sequence represents a CDNA of the invention that is differentially expressed in activated T cells
                                                                                                                                                                                                                                                                                  A---TCTTTTTAAAAAATAGTATGAATGTGAATACTAGAAAAGATTTAAAAAATAGTATG
                                                                                        TITATAGATATAATITIAATITIGITATIGGITAAGGAGACAATITITGGAGAGCAAGCAA
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Sequence 5642 BP; 1472 A; 1399 C; 1212 G; 1465 T; 0 U; 94 Other;

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96.7%;
Query Match
Best Local Similarity 98.1
Matches 3728; Conservative
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Japanese
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Best Local Similarity 99.1%;
Matches 3728; Conservative
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         1997-253003/23
                                                                Claim 1; Page 5-8;
                 P-PSDB; AAW16398
                                                neuroblastoma.
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                                              3296 TCATGTTAGCAAATGACACGTTAATATCCCTAGCAGAGGCTGTGTTCACCTTCCCTGTCG
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/product= "NOR-1 orphan receptor"
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Parkinson's disease; ss.
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     diagnosing
                                                                                                                                     This is the nucleotide sequence of a novel human neuron-derived orphan nuclear receptor gene. The open reading frame encodes a protein of 626 amino acids, which has high homology to the rat NOR-1 receptor. The protein contains several DNA binding domains including P, D and A boxes which also have high homology to the rat NOR-1 DNA binding domains. The nucleic acid and protein can be used to diagnose brain neuronal diseases, such as Alzheimer's disease, Parkinson's disease. Further, the genetic diseases can be treated using the receptor as it inhibits expression of a gene by binding to it
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Human neuron-derived orphan nuclear receptor gene - useful for brain diseases such as Alzheimer's or Parkinson's disease or
                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 3762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10;
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3762 BP; 907 A; 1128 C; 898 G; 829 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 3653.6;
Pred. No. 0;
0; Mismatches
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Milbrandt

Conneely OM,

MEDICINE

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The present sequence is that of human nor-1 nuclear receptor nucleic acid 165190. Nor-1 has been identified as a molecular target for therapeutic intervention in the treatment of myeloid leukaemia. The invention provides methods of inhibiting the proliferation of a haematopoietic stem cell or a haematopoietic myeloid cell by modulating the level of a nor-1 and/or nur77 nuclear receptor. This involves increasing the level of the receptor polypeptide or polynucleotide. e.g. by administration of a vector comprising the polynucleotide. A claimed method of treating leukaemia comprises modulating a nor-1 and/or nur77 nuclear receptor in a haematopoietic stem cell or myeloid cell. Also claimed are methods of identifying an upregulator of expression of nor-1 and/or nur77, of identifying a compound for the treatment of leukaemia, and a mouse model for leukaemia comprising a mouse having defective nor-1 and nur77 nucleic
                                                                                                                                                                                                                                                         Inhibiting proliferation of a hematopoietic cell, useful for treating or preventing leukemia, comprises modulating the level or activity of nor-1 and/or nur77 nuclear receptor.
                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 1; 101pp; English.
                                                                                                                 17-APR-2002; 2002US-0373238P.
                                                                                       15-APR-2003; 2003WO-US011804
                                                                                                                                            (BAYU ) BAYLOR COLLEGE
(UNIW ) UNIV WASHINGTON
                                                                                                                                                                                                                  WPI; 2003-854017/79.
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     Homo sapiens.
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2941 TGCTTTGTATTTAAAACAAGAACAGCCAAGGGTTGTTCGCCAGGGTAGGATGTGTTTA
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                                            TGCTTTGTATTTAAAAACAAGAACAGCCAAGGGTTGTTCGCCAGGGTAGGATGTGTCTTA
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                                                                                           Gaps
                                                                                         Indels 368;
                                                           Length 4162;
                            Sequence 4162 BP; 1017 A; 1224 C; 991 G; 930 T; 0 U; 0 Other;
                                                                                         15;
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                                                        88.4%; Score 3352; Di
90.8%; Pred. No. 0;
iive 0; Mismatches
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Matches 3779; Conservative
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Best Local Similarity
acid sequences
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Human; nor-1; nuclear receptor; receptor; leukaemia; gene therapy; cytostatic; haematopoietic cell; ds.

nuclear receptor nucleic acid 1651190.

(first entry)

12-FEB-2004 Human nor-1

BP

ADF28866 standard; DNA; 4162

Db 3661 TGTTAGCAATGACCATCAAGACTTTTAGGCCATTCTTCATGGCACCTGTCCTG 3720	RESULT 9 ABL61892 ID ABL61892 XX AC ABL61892; XZ AC ABL61892; XX AL ABL61892; XX AL ABL61892; XX XX ABL61892; XX XX XX XX XX XX XX KHuman; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; XX XX XX KHuman; cancer; colon; breast; ovary; oesophagus; kidney; thyroid; XX XX XX KM Gene; ds. XX XX XX XX XX Homo sapiens. XX
	2759 GCTCTTTTCCTTACAACCTAAAGCCAGAAACTTGCAGGGTTTTGGTTTGGTTTTTTTGTTTTTTTT

ACCTTGGCAGCACTGAGATCACGGCTACAGCCACCACGTCCCTGCCCAGCATCAGTACCT

851

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The present invention describes a method (M1) for screening for an antinoplastic agent. The method involves exposing cells to a chemical agent to be tested for antineoplastic activity, determining a change in expression of at least one gene (I) of a signature gene set, where (I) comprises a sequence (S) selected from 8447 sequences (given in ABL61664 to ABL70110), or is at least 95% identical to (S), where a change in expression is indicative of anti-neoplastic activity. (I) has cytostatic activity and can be used in gene therapy. M1 can be used for screening an anti-neoplastic agent, and can be used for producing a product which is the data collected with respect to the anti-neoplastic agent as a result of M1, and the data is sufficient to convey the chemical structure and/or properties of the agent. M1 can be used in the treatment of cancer such as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney, prostate or pancreatic cancer, adenomical cancer, infiltrating ductal cancer, infiltrating ductal cancer, infiltrating cancer, infiltrating ductal cancer, infiltrating cancer, squamous call carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilm's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cening for anti-neoplastic agent involves exposing cells to a chemical ont to be tested for anti-neoplastic activity, and determining a change expression of a gene of a signature gene set.
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                                             2000US-0235720P.
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2000US-0236028P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (Gs) identified by the chip analysis as given in the specification, and comparing the by chip analysis as given in the specification, and comparing the by chip analysis as given level in an unactivated GC, where CC dynession level to an expression level in an unactivated GC, where condulating (MS) day contacting GC with an agent that alters the modulating (MS) day contacting GC with an agent that alters the comparing cresponse in GS; (2) screening (MS) for an agent cresponse in GS; (2) screening (MS) for an agent cresponse in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, using the gene expression profile; (3) detecting (M4) an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by detecting the level of expression in a sample of the tissue of gene(s) from GS, where the level of expression of the gene is indicative of inflammation; (4) treating of expression in a subject, exposure of a subject to a pathogen or sterile inflammation (especially chronic) or in a tissue, an allergic response in a subject, exposure of a subject to a pathogen or sterile of modulating GA, M3 is useful for detecting GCA; M2 is useful for modulating GA, M3 is useful for gene that modulates the expression of gene(s) from GS in the tissue, M is useful for detecting GCA; M2 is useful for detecting GCA; M3 is useful for
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                                                                                                                                                                                                                                                                                                                                                  Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.
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                                                                                                                                                                                                                                                                   Vockley J;
                                                                                                                                                                                                                                                                     Yamaga S,
                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 800; 114pp; English
                                                                                                                                                                                                                                                                     Beazer-Barclay Y, Weissman SM,
                                                                                                                                            03-OCT-2001; 2001WO-US030821.
                                                                                                                                                                                     03-OCT-2000; 2000US-0237189P
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                                                                                                                                                                                                                                            The present invention relates to PRO proteins and their coding sequences.

The PRO proteins are useful for diagnosing and treating a B cell related disorder, eg. X-linked infantile hypogammaglobulinemia, polyasccharide antigen unresponsiveness, selective IGA deficiency, burkitt's IMT proper IGM, transient hypogammaglobulinemia of infancy, Burkitt's IMT presensitivity, rheumatoid arthritis, autoimmune mediated haemolytic anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or anytoisnin spondylitis. The PRO proteins are also useful for preparing a medicament for treating a condition that is responsive to the PRO protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO coding sequences are useful as hybridization probes in chromosome and gene mapping, in preparing PRO proteins, or in generating transgenic animals or knockout animals, which in turn are useful in the development and screening of therapeutically useful reagents.
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CTTGGCGCCCGGCTGCATCGCACCCGGCCGCTGCTGGACCCGGCGGTGAAGGCGGTCC
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This invention relates to the novel association of protein sequences (and the genes which encode them) to the NF-kappaB pathway. The invention may be useful for the production of compounds with an antinflammatory, cytostatic, hepatotropic, virucide, antiarthritic, antinflammatory, cytostatic, hepatotropic, virucide, antiarthritic, antinflammatory, cytostatic, hepatotropic, inmunosuppressive or vulnerary activity or for gene therapy. The proteins and nucleotides are useful for diagnosing, preventing, treating, or ameliorating conditions or diseases associated with the NF-kappaB pathway. The condition is an immune disorder, an inflammatory disorder.

CC diseases associated with the NF-kappaB pathway. The condition is an immune disorder, an inflammatory disorder.

CC diseases associated with the NF-kappaB pathway. The condition is an immune disorder, an inflammatory disorder in inflammatory disorder in the patic disorders, Hodgkin's lymphomas, haematopoietic tumours, hyper-IgM syndrome, hypohidrotic ectodermal dysplasia, x-linked anhidrotic conformal dysplasia, immunodeficiency, viral replication, host cell converting by the patities of immune responses, rheumatoid arthritis, inflammatory bowel disease, colitis, asthma, atherosclerosis, cachexia, euthyroid sick syndrome, stroke, BAE, autoimmune disorders, disorders related to aberrant acute phase responses, hypercomenical conditions related to organ transplant conditions, blirth defects, necroic lessions, wounds, crycumonenical conditions related to organ transplant concers and HIV propagation in cells infected with other viruses. The present sequence is that of a human gene which is necessing hypering by the inch hy, the index of the novel association with the NF-kappaB pathway of the liventh hypering hypering and the paper in the specification but appear in the specification but
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                                                                                                                                                               New isolated polynucleotides and polypeptides associated with NF-kappaB pathway, useful for diagnosing, treating, or preventing disorders or diseases associated with NF-kappaB pathway.
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                                               Carman J;
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                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 63; 237pp; English.
                                               Feder JN,
(BRIM ) BRISTOL-MYERS SQUIBB CO
                                               Neubauer
                                                                                         WPI; 2004-562168/54.
P-PSDB; ADR14063.
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2170 1810 1270 1330 1390 1450 1510 1570 1630 1690 633 693 753 813 873 933 993 GAAACCGATGTCAGTACTGTCGATTTCAGAAGTGTCTCAGTGTTGGAATGGTAAAAGAAG TIGITCCGTACAGATAGTCTGAAAGGGAGGAGGACGTCGTCTGCCTTCCAAACCAAAGAGCC 1234 CATTACAACAGGAACCTTCTCAGCCCTCTCCACCTTCTCCCAATCTGCATGAATG TCCCCAAAGAAGATCAGACATTACTTATTGAATCAGCCTTTTTTGGAGCTGTTTGTCCTCA 1534 GACTTTCCATCAGGTCAAACACTGCTGAAGATAAGTTTGTGTTCTGCAATGGACTTGTCC 574 CCTCGGCGCCCGGCTGCATCGCACCCGGCCCGCTGGACCCGCCGATGAAGGCGGTCC CCGCGCCCAGCCCGGCCGGCCACCACCTCGGCTACGACCCGACGGCCGCTGCCGCGC AGAAAAATGCAAAATATGTTTGCCTGGCAAATAAAAACTGCCCAGTAGACAAGAGACGTC 1054 AGAAAAATGCAAAATATGTTTGCCTGGCAAATAAAACTGCCCAGTAGACAAGAGAGGTC 1751 GAAACCGATGTCAGTACTGTCGATTTTCAGAAGTGTCTCAGTGTTGGAATGGTAAAAGAAG crerigicedagerriaacadacieaacaccadadarerreariarriceadaraciere TGACAGCCTCCATTGATGTATCCAGAAGCTGGGCAGAAAAAAAGATTCCGGGATTTACTGATC TGACAGCCTCCATTGATGTATCCAGAAGCTGGGCAGAAAGATTCCGGGATTTACTGATC 454 CCAGCCCGGAGGACGAGGTGCTGCCCAGCACCTCCATGTACTTCAAGCAGTCCCCACCGT 514 CCACCCCCACCACCACCGGGGGCCTTCCCCCCGCAGGCGGGGGGTTTTGGGACGAGGGCACTGC CCTCGGCGCCCGGCTGCATCGCACCCGGCCCGCTGCTGGACCCCGCCGATGAAGGCGGTCC CCACGGTGGCCGGCGCGCGCTTCCCGCTTCCACTTCAAGCCCTCGCCGCCGCATCCCC CCACGGTGGCCGGCGCGCGCTTCCGCTTCAAGCCCTCGCCGCGCATCCCC TCAGCCTGCCGCTGGGAGCCGCAGCCGCGGGGAGCCAGGCCAGGCCGCGCGCTTGAGAGCC TCACGCCTCCCCTACCGCGTCCAGCCTGCTGGGCGAGAGTCCCAGCCTGCCGTCGCCGC 874 TCACGCCCTCCCCTACCGCGTCCAGCCTGCTGGGCGAGAGTCCCAGCCTGCCGTCGCCGC CCAGCAGGAGCTCGTCTCGGCGAGGCACGTGTGCCCGTGTGCGGGGACAACGCCGCCT ccadcadedacercercercededadedecacerciecedererecededacaacaacecerce GCCAGCACTACGGCGTGCGAACCTGCGAGGGCTGCAAGGGCTTTTTCAAGAGAACAGTGC TTGTCCGTACAGATAGTCTGAAAGGAGGAGGAGGTCGTCTGCCTTCCAAACAAGAGCC CATTACAACAGGAACCTTCTCAGCCCTCTCCACCTTCTCCTCCAATCTGCATGAATG CCCTTGTCCGAGCTTTAACAGACTCCAACACCCCAGAGATCTTGATTATTCCAGATACTGTC CCACTGACCAGGCTGCTGCAGGCACAGATGCTGAGCATGTGCAACAATTCTACAACCTCC TCCCCAAAGAAGATCAGACATTACTTATTGAATCAGCCTTTTTTGGAGCTGTTTGTCCTCA GACTITICCATCAGGICAAACACTGCTGAAGATAAGITTGTGTTCTGCAATGGACTTGTCC 1294 1414 1391 1871 1354 2111 1331 1511 1691 1811 1174 1931 1991 2051 1151 1211 1271 634 694 754 1571 934 1631 994 1114 g 셤 8 8 g g В ò 유 셤 g 셤 셤 à g g q à g ò 셤 ò ò 8 ð ò q ò ò ò ò ઢ 8 ₹ ò 1030 1150 1090 393 453 ACCACCACCACCACCATCATCACCAGCAGCAGCATCAGCATCCATTCCTCCAGCCT CCAGCCCGGAGGACGAGCTGCCCAGCACCTCCATGTACTTCAAGCAGTCCCCACCGT

	RESULT 13 AD131602 XX XX AD131602; XX C AD131602; XX XX Human cDNA #928. XX How sapiens. XX
231 TGCATCGACTTCAGTGCCTTCGTGGATTTGGGGACTCGTCTATTAAAGACTTTT 2290 1594 TGCATCGACTTCAGTGCCTTCGTGGATTTGGGGACTCGCTCTATTAAAGACTTTT 1653 2291 CCTTAAATTTGCAGACCTCGAACCTTGATTACCAGCTCTGCTGCTGCTGCACTGTTTT 1653 2291 CCTTAAATTTGCAGAGCTGAACCTTGATATCCAAGCTTAGCCTGCTGCACTGCACTGA 2350 1654 CCTTAAATTTGCAGAGCTGAACCTTGATATCCAAGCCTTAGCCTGCTGCACTGAACTAGATTTGTAGAACTTGAACAAGAGATTAAAAGAACCTAGAAGAATTTGAACAAGACTTTAAAAGAACCACCAAGAAATTTGAAAATTGAAACAACAATTAAAAGAACAACAAAAAAAGAAAATTGAAAAAAAGAAAATTAAAAAAAA	2771 ACAACCTAAAGCCAGAAAACTTGCAGAGTATTGTGTGGGGGTTGTTTTATTTA

The invention relates to a composition comprising a plurality of cDNAs for detecting the altered expression of genes in an immunological cordetecting the altered expression of genes in an immunological condition also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, comparising obtaining nucleic acids from a sample, contacting the nucleic acids of the sample with an array comprising the plurality of cDNAs under conditions to form one or more hybridisation complexes, detecting the hybridisation complexes and comparing the plurality of cDNAs under conditions complexes with the level of hybridisation complexes with the level of hybridisation complexes or detected in a non-diseased sample, where an altered level of the detected hybridisation complexes correlates with the presence of an immunopathological condition. Also disclosed are an expression profile comprising a microarray and a plurality of detectable complexes and a method for identifying a plurality of polynucleotide probes. The cDNAs are useful as hybridisable array elements in a microarray for monitoring the expression of target polynucleotides. The microarray for monitoring the expression of target polynucleotides. The microarray can be used in drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. The composition and also be used in drug discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. The composition may also be used in purification of a subpopulation of maxing directly for the treatment of the discovery and development, toxicological and carcinogenicity studies, forensics or pharmacogenomics. The composition may also be used in purification of a subpopulation of maxing directly formed to the printed specification but was obtained in electronic format directly formed but we have a part of the discovery and development of the discovery and development of the discovery and development of the d from USPTO at segdata.uspto.gov/sequence.html. NO 928; 50pp; English Π SEO Claim 1;

Sequence 2714 BP; 596 A; 924 C; 680 G; 514 T; 0 U; 0 Other;

DB 11; Length 2714;

ö 138 251 78 TCACTCGCACACACACACACACGCGCACACACGCCTCCGCCACACTTCGCTCTCCC CGCCCCTCCCGGGCTCACTTTGCAACGCTGACGGTGCCCGCAGTGGCCGTGGAGGTGGGA Gaps ö 4; Indels Query Match

70.9%; Score 2689.6;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2692; Conservative 0; Mismatches 132 252 19 79 139 192 8 6 8 6 ð ద 8 6

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Pred. No. 0;
0; Mismatches 535; Indels
                                                                                                                                                                                                              "rat nuclear receptor"
                                                                                     cerebral neuron nuclear receptor gene
               BP.
              4400
                                                                                                                                                                       Location/Qualifiers 700. .2586
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               mRNA;
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               standard; cDNA to
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Best Local Similarity 83.4°
Matches 3131; Conservative
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1438 CORGETTOCCCCTTGGCCAACAAGGGCCCCCGCTTGCCTTCCCCCCTTCCCCTCTCCCCCTCCCCCTCAACACAACA
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310 GCAGCGGAGAACTGGACG-CTGGGGAACCTCTGGGGGGCCTCTCCCATGAACTGGGACGCGTGTGAACTGGCACGCGGGGGGGCGTTGTAACACCCGGGGGGGG

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3591 CGATCAAGGGTTAACCCTAGGAGAACATGCAAATAAGTAGGAACTGGGTCAGACAGGGTA 3650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel targeting construct for producing transgenic mouse useful as disease model and for identifying modulators of gene expression, has sequences homologous to neural orphan receptor 1 and a selectable marker.
                                                                                                                                                                                                                                                        Murine; NOR1; neuroleptic; Neural Orphan Receptor 1; Translocated in Extraskeletal Chondrosarcoma; TEC; cell proliferation; apoptosis; central nervous system; transgenic mouse; pain response threshold; impaired balance; impaired motor coordination; gene; ds.
                                   Indels
                                                                                                                                                                                                                                      coding sequence
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                                                                                TTAAGGAGACAATTTTGGAGGAGCAAGCAAATCTTTT
                                                                                              TTA--TAGACAATTTTGGAAAGCAAGAGAATCATCT
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65.9%; Score 2500; DE
Best Local Similarity 83.4%; Pred. No. 0;
Matches 3131; Conservative 0; Mismatches
                                                                                                                                                                                                                                    Murine Neural Orphan Receptor 1; NOR1,
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24-SEP-2001; 2001US-0324614P.
04-DEC-2001; 2001US-00005169.
                                                                                                                                                                 DNA; 4400
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P-PSDB; ABB98438.
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                                                          GGATGGGGTGGGAGGGGGT--TATACTTCATGAGGTTTTCTAAGAAATTGCTAACAAGG
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22; The present sequence is a coding sequence for murine Neural Orphan Receptor 1 (NOR1). NOR1, also known as Translocated in Extraskeletal Chondrosarcoma (TEC), is involved in the control of cell proliferation and apoptosis and is expressed mainly in the central nervous system. The NOR1 coding sequence was used to generate a targeting construct (I). (I) is useful for producing a transgenic mouse comprising a disruption in a NOR1 gene and exhibiting increased or enhanced pain response threshold, or impaired balance and impaired motor coordination Gaps 90; Sequence 4400 BP; 1055 A; 1239 C; 1034 G; 1072 T; 0 U; 0 Other; Length 4400;

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Copyright (c) 1993 - 2005 Compugen Ltd.
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RESULT 1 US-09-949-016-3789 ; Sequence 3789, Appli ; Patent No. 6612339 ; GENERAL INFORMATION: ; TITLE OF INVENTION: ; FILE REPERENCE: CLO. ; CURRENT APPLICATION NO. ; PRIOR FILING DATE: ; PRIOR FILING DATE: ; PRIOR FILING DATE: ; PRIOR FILING DATE: ; RIOR PRIOR DATE: ; RIOR FILING DATE: ; RUMBER OF SEQ. ID NO.	ULT 1 09-949-016-3789 equence 3789, Applicat atent No. 6812339 ENERAL INFORMATION: ATITLE OF INVENTION: FILE REFERENCE: CLOOIS CURRENT APPLICATION NU CURRENT APPLICATION NU PRIOR APPLICATION NUM PRIOR APPLICATION NUM PRIOR FILING DATE: 20 PRIOR APPLICATION NUM PRIOR FILING DATE: 20 PRI	5-378 789, 789, 700MA 700MA 700MA 700MA 700MA 710MA 710MG 71	9 AADD11 TION: TIER, TICON: TICON: TOPE: DATE: TON N AATE: TON N AATE: TON N AATE:	ULT 1 09-949-016-3789 equence 3789, Application US/0994901 atent No. 6812339 APPLICANT INFORMATION: TITLE OF INVENTION: POLYMORPHISMS IN TITLE OF INVENTION: POLYMORPHISMS IN TITLE OF INVENTION: WITH HUMAN DISE FILE REFERENCE: CLOO1307 CURRENT APPLICATION NUMBER: 60/09/1759 PRIOR PEDLICATION NUMBER: 60/21,755 PRIOR APPLICATION NUMBER: 60/231,768 PRIOR APPLICATION NUMBER: 60/231,768 PRIOR FILING DATE: 2000-10-03 PRIOR FILI	US/ B B B B B B B B B B B B B B B B B B B	GNMENTS KNOWN GENES ASS ASE, METHODS OF 9,016 9,016	ASSOCIATED OF DETECTION AND USES		THERE
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Qy 3601 CATGCAAATCAGCAGGAACTGGTCATACAGGGTAAGCACCAGGGACAATAAGGATTTTTA 3660 Db 3601 CATGCAAATCAGCAGGAACTGGTCATACAGGGTAACCACCAGGGACAATTTTTA 3660 Qy 3661 TAGATATAATTTTTGTTATTGGTTAAGGACAATTTTGGAGGCAAGCAA	RESULT 2 US-09-949-016-905 US-09-949-016-905 ; Sequence 905, Application US/09949016 ; Patent No. 6812339 ; GENERAL INFORMATION: ; APPLICANT: VENTER, J. Craig et al. ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF; ; FILE REPERENCE: CL001307 ; CURRENT FILING DATE: 2000-04-14, 755 ; PRIOR APPLICATION NUMBER: 60/241, 755 ; PRIOR PILION DATE: 2000-07, 70, 70, 70, 70, 70, 70, 70, 70, 70,	PRIOR FILING DATE: 2000-10-03 PRIOR FILING DATE: 2000-10-03 PRIOR APPLICATION NUMBER: 60/231,498 PRIOR PILING DATE: 2000-10-03 SOFTWARE: FactSEQ for Windows Version 4.0 SOFTWARE: FactSEQ for Windows Version 4.0 TYPE: DNA ORGANISM: Human US-09-949-016-905 Query Match SEQ 10 09 98.1%; Score 3722; DB 4; Length 3802;	Best Local Similarity 99.4%; Pred. No. 0; Matches 3779; Conservative 0; Mismatches 15; Indels 8; Gaps 4; Qy	Db 121 CACCGGCTCCCTCACTCGAACACACACACGCCCACACACT
2521 CTCCAGCGCATCTTCTACCTGAAGCTGGAAGACTTGGTGTCTCCACCTTCCATCATTGAC 2580 2521 CTCCAGCGCATCTTCTACCTGAAGCTGGAAGACTTGGTGTCTCCACCTTCCATCATTGAC 2580 2581 AAGCTCTTCCTGGACCTACCTTCTAATCAGGAGCAGTGGAGCAGTGAGCTCCTCCACTTGATCACTGAACTTGCAACTGAACTTCCTC 2640 2581 AAGCTCTTCCTGGACCACCTTCTTTTTTTCTG 2580 2641 TCTCCTAGCACCTGCTTGCTACCTTTCTAATCAGGAGCAGTGGAACCTATCATTTCCTG 2700 2641 TCTCCTAGCACCTGCTTGCTACGAAGGATAGGTTTGGAAACCTATCATTTCCTG 2700 2641 TCTCCTTAAGAGGAAAAGCAGCACAAGAGATTGGAAACCTTTTTTTT	2761 TCTTTCCTTACAACCTAAAGCCAGAAACTTGCAGGGATTGTGTTGGGGTTGTTTT 2820 2761 TCTTTTCCTTACAACCTAAAGCCAGAAAACTTGCAGAGTATTGTGTTGGGGTTGTGTTTT 2820 2821 ATATTTAGGCATTGGGGGTGGGGTGGGGGTTATAGTTCATGAGGGTTTTCTAAGA 2880 2821 ATATTTAGGCATTGGGGGTGGGGTGGGGGTTATAGTTCATGAGGGTTTTCTAAGA 2880 2881 AATTTAGGCATTGGGGGTGGGGTGGGGGTTATTGTTCATGAGGGTTTTCTAAGA 2880 2881 AATTGCTAACAAGCACTTTTGGACAATGCTATCCCAGCAGGAAAAAAAGGATAATATA 2940 2881 AATTGCTAACAAAGCACTTTTGGACAATGCTATCCCAGCAGGAAAAAAAGGATAATATA 2940 2941 AATTGCTAAAACTCTTTTGGACAATGCTATCCCAGCAGGAAAAAAAGGATAATATA 2940	ACTGITITADA ACTCITICIGGGGGATCCAATTATAGITGCTITGTATTAAAAACAAGA ACGCCAAGGGTTGTTCGGGGGATCCCAATTATAGITGCTTTTGTATTTAAAAACAAGA ACAGCCAAGGGTTGTTCGCCAGGGTAGGATGTCCTTAAAGATTGGTCCTTGAAAATAT ACAGCCAAGGGTTGTTCGCCAGGGTAGGATGTCTCTTAAAGATTGGTCCTTAAAGATTGTCCTTTTAAAAATTTC CTTCCTGTATCAAAGGTACGTATGTGGTGGTAACAAGGCAAAACTTCCTTTTAATTTC CTTCTCTGTATCAAAGGTACGTATGTGGTGCAAACAAGGCAAAACTTCCTTTTAATTTC CTTCTTCCTTTATTTTAACAAATGGTGAAAGAACAAGGCAGAAACTTCCTTTTAATTTC CTTCTTCCTTTATTTTAACAAATGGTGAAAAAAAGGCAAAACAAAAAAAGGCAAAACAAAAAAAA	CTICTICCTTTATTTTAACAAATGGTGAAAGATGGAGTTACCTACAAATCAGACATGG CAAAACAATAATGGCTGTTTGCTTCCATAAACAAGTGCAATTTTTTAAAGTGCTGTCTTA	3361 TTGGGGGTATGGCCCTCCTAGCGGGGCTGTGTTCCTCCTGCCGGTCCC 3360 3361 TTCTGAGGTATGGCCCATCCAGGACTTTTTGGCCATTCTTGATGGAACCCTGCCGGTCCC 3420 3361 TTCTGAGGTATGGCCCATCCAGGACTTTTTGGCCATTCTTGATGGAACCCGGTCCTGCC 3420 3421 CTGACTGTCCTGCAACTGGATCAGATTATAACTGGATTACATGTAACTGTT 3480 3421 CTGACTGTCCAGCCATCCTGAAGTGGATTATAACTGGATTACATGTT 3480 3421 TTGGTTGTTCTATCCACCCCACCGAGGTTCCCTAACTTGCTTCAGTTAACTGTT 3480 3481 TTGGTTGTTCTATCAACCCCACCAGAGTTCCCTAACTTGCTTCAGTTATAACTGT 3540 3481 TTGGTTGTTCTATCAACCCCACCAGAGTTCCCTAACTTGCTTCAGTTATAACTAGTAACTG 3541 ACTGGTAATTCATTCAACACCCCACCAGAGTTCCCTAAGTTTTGATCCCTAAGTAACTG 3541 ACTGGTAATTCATTCAACACCCCACCAGAGTTCAGTTTTGATCCCTAAGTAAG

1499 CGCCTCTCGGCCTCCCCTACCGCGTCCAGCCTGCTGGCGAGAGTCCCAGCC 1518	1739 ACAAGAGACGTCGAAACCGATGTCAGTACTGTCGATTTCAGAAGTGTCTCAGTGTTGGAA 1798	1919 GCATGATGACTTGCCGAGCTTTAACAGACTCAACACCCAGAGATCTTGATTATT 1978	210 215 216 221 222	2219 ATGGACTTGTCCTGCATCGACGCCTTCGTGGATTTGGGGAGTGGCTCGACTCTA 2278 [1341 TGTCAGCACTGAGCATGATCACGGAAGGTTTAAAGAACCAAAGAGAGTCGAAG 2400 2399 AGCTATGCAACAAGATCACAAGCATTTAAAAGACATCAGAAGCACGCAC
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3721 AATCTTCTTTTAAAAAATAGTATGAATGTGAATACTAGAAAAGATTTAAGAAATAGTAT 3780
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                  us-09-023-655-928

Sequence 928, Application US/09023655

Patent No. 6607879

GENERAL INFORMATION:

APPLICANT: Cocke, Benjamin G.
APPLICANT: Susan G. Stuart

APPLICANT: Osffrey J. Sellhamer

TITLE OF INVENTION: COMPOSITION FOR THE DE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508

CORRESPONDENCE ADDRESS:
ADDRESSEE: INCTTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 9430A
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Pred. No. 0;
0; Mismatches
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                                                                                                   3781 GAGTGTGAGTACTAGGAAGGAT 3802
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
ATTORNEY/AGENT INPORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-OG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 845-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 928:
SEQUENCE CHARACTERISTICS:
LENGTH: 2774 base pairs
                                                                                   3773 GAGTGTGAGTACTAGGAAGGAT
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 99.9°
Matches 2692; Conservative
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STRANDEDNESS: single
TOPOLOGY: linear
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LIBRARY: GENBANK
CLONE: 9131757
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; CLONE: 91311504
US-09-023-655-928
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2641 CCTCTCCTAGCACCCTGCTTCTACGCAGCAAGGGATAGGTTTGGAAACCTATCATTCC
                                                                                                             TAACTGTTTTAAAACTCTTTCTGGGGAATCCAATTATAGTTGCTTTGTATTAAAAACAA
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                                         CCTCTCCTAGCACCTGCTTGCTACGCAAAGGGATAGGTTTGGAAACCTATCATTTCC
                                                                                              GCTCTTTTCCTTACAACCTAAAGCCAGAAAACTTGCAGAGTATTGTGTTTGGGGGTTGTGT
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                                      CAGGGTAGGATGTCTTTAAAGATTGGTCCCTTGAAAATATGCTTCCTGTATCAAAGGTA
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TULE BEFERENCE: CLOO1307
CURRENT PILLING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/231,768
FRIOR PILLING DATE: 2000-10-03
FRIOR PILLING DATE: 2000-10-03
FRIOR FILLING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 12647
LENGTH: 47184
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          CAAGGTCCTGGGTGCCCTGGTAGAACTGAGGAAGATCTGCACCCTGGGCCTCCAGGGCTT
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US-09-949-016-12647
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US-09-949-016-12647
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US-09-023-655-1400

| Sequence 1400, Application US/09023655
| Patent No. 6607879
| GENERAL INFORMATION:
| APPLICANT: Cocks, Benjamin G. APPLICANT: Susan G. Stuart
| APPLICANT: Susan G. Stuart
| APPLICANT: Useffrey J. Seilhamer
| TITLE OF INVENTION: COMPOSITION FOR THE DETI:
| TITLE OF INVENTION: EXPRESSION
| NUMBER OF SEQUENCES: 1508
| CORRESPONDED ADDRESSEBS: INCTTE PHARMACEUTICALS, INC. STREET: 3174 PORTER DRIVE
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GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUWAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/237,768
FRIOR PALICATION NUMBER: 60/237,768
FRIOR PELING DATE: 2000-10-03
FRIOR PELING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOUTHER OF SESCION WINDOWS VERSION 4.0
SEQ ID NO 15531
LENGTH: 47184
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                               Length 47184;
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                                                                                                               Sequence 15531, Application US/09949016
Patent No. 6812339
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Best Local Similarity 99.7%;
Matches 1434; Conservative (
                                                                                   RESULT 5
US-09-949-016-15531
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Pred. No. 3.7e-105;
0; Mismatches 640; Indels 144;
                                                                                                       COMPOTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IPOPY disk
COMPUTER: PLOPSY disk
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
NAME: Zeller, Karen J.
REGISTAATION NUMBER: 37,071
REGISTAATION NUMBER: 37,071
RECECHONE: (650) 855-055
TELECHONE: (650) 855-0555
TELEPHONE: (650) 855-0555
INFORMATION FOR SEQ ID NO: 1400:
SEQUENCE CHARACTERISTICS:
LENGTH: 3427 base pairs
TYPE: nucleic acid
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US-09-023-655-1400
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US-09-949-016-828

Sequence 828, Application US/09949016

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Sequence 828, Application US/09949016

Sequence 828, Application US/09949016

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WIMBER: 60/241,755

FILE REFERENCE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR PLING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SSOFTWARE: FastSEQ for Windows Version 4.0

SSO ID NO 828

LENGTH: 3327
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Fater No. 681239

GENERAL INFORMATION:
PAPELCANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT FILING DATE: 2000-04-14

FRIOR FILING DATE: 2000-04-14

FRIOR APPLICATION NUMBER: 60/231,768

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-09-08

WINNBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NOS: 207012
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APPLICANT: Sakurada, Kazuhiro
APPLICANT: Palmer, Theo
APPLICANT: Palmer, Theo
APPLICANT: GAGE, Fred H.
TITLE OF INVENTION: REGULATION OF TYROSINE HYDROXYLASE
TITLE OF INVENTION: RYRESSION
FILE REFERENCE: 0725/031001;
CURRENT APPLICATION NUMBER: US/09/277,078
CURRENT FILING DATE: 1999-03-26
NUMBER OF SEQ ID NOS: 60
SOFTWARE: FastSEQ for Windows Version 4.0
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Pred. No. 7.9e-103;
0; Mismatches 671;
   GAGATCTTGATTATTCCAGATACTGTCC-
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Patent No. 6312949
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Best Local Similarity 58.1%;
Matches 1105; Conservative (
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ORGANISM: Rattus norvegicus
FEATURE:
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Fatent No. 6812339
GENERAL INFORMATION:
APPLICANT: VERYTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241.755
RIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/231,498
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PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PSEKSEQ for Windows Version 4.0
SEQ ID NO 4392
LENGTH: 2486
                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-4392
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US-US-343-ULB-35444, Application US/09949016

| Sequence 35444, Application US/09949016
| Patent NO. 681239
| GENERAL INFORMATION:
| TITLE OF UNIVENTION: POLYMORPHISM IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: POLYMORPHISM IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WIMBER: US/09/949,016
| TITLE OF INVENTION NUMBER: US/09/14,755
| PRIOR PELICATION NUMBER: 60/241,755
| PRIOR PILING DATE: 2000-10-20
| PRIOR PILING DATE: 2000-10-03
| PRIOR PILING DATE: 2000-10-03
| PRIOR PILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SEQ ID NO 35444
| LENGTH: 601
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Pred. No. 2:2e-63;
1; Mismatches 0;
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US-09-949-016-35444
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                                                                                                                                 GGGCCTCCAGCGCATCTTCTACCTGAAGCTGGAAGACTTGGTGTCTCCACCTTCCATCAT 2576
                                                                                                                                                             GGAGCCCACCGAGTCCAAGGTCCTGGTGCCCTGGTAGAACTGAGGAAGATCTGCACCCT 2516
                                                              1774 AGCCAGCTGCCTGTCACTTTGGGCAAACTGCCCGAGCTGCGGACCCTGTGCACCCA 1833
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                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 58, Application US/09566921
; Sequence 58, Application US/09566921
; Patent No. 668288
; GENERAL INFORMATION:
APPLICANT: Loring, Jeanne F.
APPLICANT: Loring, Jeanne F.
APPLICANT: Edwards, Carla M.
APPLICANT: Edwards, Carla M.
TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
FILE REPERBURE: PA-0024 US VO9/566,921
CURRENT APPLICATION NUMBER: US/09/566,921
CURRENT FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 138
SOFTWARE: PERL PROGRAM
SEQ ID NO 58
ILENGTH: 2637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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; OTHER INFORMATION: Incyte ID No. 6682888 127112.18
US-09-566-921-58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.0%; Score 340.6; DB 4;
61.3%; Pred. No. 7.1e-69;
tive 0; Mismatches 389;
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Best Local Similarity 61.33
Matches 663; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                    RESULT 11
US-09-566-921-58
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gequence 35441, Application US/09949016

gequence 35441, Application US/09949016

general No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 2007012

SOFTWARE: FESEUSE for Windows Version 4.0

LENGTH: 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    366 CAGAAAGACATGGGTTAAAAGAACCAAAGAGTGGAAGAGGTATGCAAAGACAACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         486 TGGGTGCCCTGGTAGAACTGAGGAAGATGTGCACCCTGGGGCCTCCAGCGCATCTTCTACC
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                   3763 AAAATAGTATGAGTGTGAGTACTAGGAAGGAT 3794
                                     301 RAAATAGTATGAGTGTGAGTACTAGGAAGGAT 332
                                                                                                              RESULT 14
US-09-949-016-135236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-135236
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US-09-949-016-35441
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Sequence 135237, Application US/09949016

Sequence 135237, Application US/09949016

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 135237

LENGTH: 601
                                                                                                                                                   ATCCCTAGATAAGAACATGCAAAATCAGCAGGAACTGGTCATACAGGGTAAGCACCAGGGA 3645
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                                                                                                                                                                                                                          3646 CAATAAGGATTTTTATAGATATAATTTTAATTTTTGTTATTGGTTAAGGAGACAATTTTGG 3705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 CAATAAGGATTTTTATAGATATATAATTTTAGTTATTGTTATTGGTTAAGGAGACAATTTTTGG 240
                                                                                              CAGTTATAGTAACTGACTGGTATATTCATTCAGAAGCGCCATAAGTCAGTTGAGTATTTG 120
                                                                                                                                                                       121 ATCCCTAGATAAGAACATGCAAAATCAGCAGGAACTGGTCATACAGGGTAAGCACCAGGGA 180
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                                     1 TracardraacrdrivingGridicircrarcaaccccacagagricccraaacrigcri
                                                                        3526 CAGTTATAGTAACTGACTGGTATATTCATTCAGAAGCGCCATAAGTCAGTTGAGTATTTG
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98.8%; Pred. No. 2.2e-63;
tive 1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                             3763 AAAATAGTATGAGTGTGAGTACTAGGAAGGAT 3794
                                                                                                                                                                                                                                                                                                                                                                                                   Query Match . 8.3'
Best Local Similarity 98.8'
Matches 328; Conservative
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US-09-949-016-135237
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3466
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                          Query Match 4.6%; Score 174.6; DB 4; Length 601; Best Local Similarity 99.4%; Pred. No. 1.36-30; Matches 174; Conservative 1; Mismatches 0; Indels 0;
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-35441
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Gaps

Search completed: March 21, 2005, 20:50:42 Job time : 606 secs

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March 21, 2005, 17:28:21 ; Search time 2013 Seconds (without alignments) 11220.332 Million cell updates/sec
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2: /cgn2_6/ptodata/1/pubpna/PCT_MEW_PUB.seq:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5544816 seqs, 2976611598 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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3794
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		de			SUMMARIES	
Result No.	Score	Ouery Match	Query Match Length DB	DB	ID	Description
1	3794	100.0	3794	18	US-10-608-863-1	Sequence 1, Appli
8	3722	98.1	3802	σ	US-09-853-386-46	Sequence 46, Appl
m	3722	98.1		σ	US-09-853-386-78	Sequence 78, Appl
4	3722	98.1		17	US-10-414-080-1	Sequence 1, Appli
ß	3722	98.1	3802	19	US-10-659-004-115	Sequence 115, App
9	3679.2			16	US-10-247-671-105	Sequence 105, App
7	3668.2			13	US-10-002-600-53	Sequence 53, Appl
80	2875			10	US-09-873-367C-229	Sequence 229, App
σ	2875			18	US-10-755-889-63	Sequence 63, Appl
10	2689.6			17	US-10-641-643-928	Sequence 928, App
11	2500			σ	US-09-853-386-47	Sequence 47, Appl

Sequence 3, Appli Sequence 2, Appli	3 205	57,	ω,	52		Sequence 55, Appl	,	14,	565	Sequence 94, Appl	Seguence 56, Appl	Sequence 4, Appli	Sequence 253, App	Sequence 46, Appl	ч	Н	3, 4	Sequence 101, App	Seguence 24, Appl	-	500,	11,	σ	ñ	Seguence 3, Appli	Sequence 45, Appl	Seguence 90, Appl	Seguence 872, App	ď	51, 7		Sequence 8211, Ap
13 US-10-005-169-3 17 US-10-414-080-2	17 US-10-191-803-209	9	17 US-10-414-080-8	Þ	13 US-10-005-169-1	9 US-09-853-386-55	17 US-10-414-080-6	9 US-09-853-386-14	18 US-10-723-860-5653	15 US-10-205-951-94		9 US-09-853-386-4		15 US-10-205-951-46		17 US-10-641-643-1400		16 US-10-247-671-101	9 US-09-853-386-24		17 US-10-388-934-500	18 US-10-664-705-11	9 US-09-853-386-29	15 US-10-205-951-71	9 US-09-853-386-3	15 US-10-205-951-45	9 US-09-853-386-90	10 US-09-960-706-872	17 US-10-414-080-29	9 US-09-853-386-51	17 US-10-414-080-4	17 US-10-131-827-8211
4400	4400	5115	5115	1884	1884	1606	1606	3421	3471	2799	3421	3427	3427	3427	3427	3427	3427	3436	2154	2154	2002	2002	2247	2247	2458	2458	2469	2469	2469	433	433	069
65.9 65.9	62.9	62.5	62.5	39.5	39.2	27.0	27.0	13.2	13.2	13.1	13.1	13.1	13.1	13.1	13.1	13.1	13.1	13.1	13.1	13.1	13.0	13.0	13.0	13.0	13.0	13.0	12.4	12.4	12.4	11.2	11.2	11.0
2500	2500	2371	2371	1485.6	1485.6	1022.8	1022.8	499.6	499.4	497	497	497	497	497	497	497	497	497	496	496	492.8	492.8	492.4	492.4	492.4	492.4	469.4	469.4	469.4	426.4	426.4	418.4
12	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	c 43	C 44	45

ALIGNMENTS

Sequence 1, Application US/10608863; Publication No. US20040214192A1; GENERAL INFORMATION:

US-10-608-863-1

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APPLICANT: Kagaya', Shinji
APPLICANT: Yayoi, Yoshihiro
APPLICANT: Yayoi, Yoshihiro
APPLICANT: Saito, Hirohisa
TITLE OF INVENTION: ALLERGIC DISEASES, AND DRUGS FOR TRE.
TITLE OF INVENTION: ALLERGIC DISEASES
TITLE OF INVENTION: ALLERGIC DISEASES
TITLE OF INVENTION: ALLERGIC DISEASES
FILE REFERENCE: 3462.1003-000
CURRENT APPLICATION NUMBER: US/10/608,863
CURRENT APPLICATION NUMBER: US/202-188490
PRIOR APPLICATION NUMBER: JD 2002-188490
PRIOR APPL
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	AAGCAAATCT AAGCAAATCT ATGAGTGTGA ATGAGTGTGA	APPLICANT: Breenihan, Barry APPLICANT: Conneely, Oliver APPLICANT: Conneely, Oliver APPLICANT: Fitzgerald, Oliver TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors FILE REFERENCE: P01972US1 CURRENT FILLING DATE: 2001-05-11 PRIOR APPLICATION NUMBER: US 60/203645 PRIOR APPLICATION NUMBER: US 60/203645 PRIOR APPLICATION NUMBER: US 60/203645 NUMBER OF SEQ ID NOS: 153 SEQ ID NO 46 LENGTH: 3802 TYPE: DAA TYPE: DAA CORGANISM: HUMAN	Query Match 98.1%; Score 3722; DB 9; Length 3802; Best Local Similarity 99.4%; Pred. No. 0; 0.0.0; Matches 3779; Conservative 0; Mismatches 15; Indels 8; Gaps 4; Oy 1 ATAAATGACGGCGGGGGGGGGGGGGGGGGGGGGGGGGGG
2221 GGACTTGTCCTGCATCGATGCCTTCGTGGATTTGGGGAGTGGCTCGACTCTATT 2280 2281 GGACTTGTCCTGCATCGACTTCAGTGCCTTCGTGGATTTGGGGAGTGGCTCGACTCTATT 2280 2281 AAAGACTTTCCTTAAATTTGCAGAGCCTGAACCTTGATATCCAAGCCTTGCTGCTGCTG 2340 2281 AAAGACTTTCCTTAAATTTGCAGAGCCTGAACCTTGATATCCAAGCCTTAGCTGCTGCTG 2340 2341 TCAGCACTGAGCATCACAGAAAGACCTTGATATCCAAGAGTCGAAGAG 2400 2341 TCAGCACTGAGCATGATCACAGAAAGACTTAAAAGAACCAAAGAGAGTCGAAGAG 2400 2401 CTATGCAACAGATCACAGAAAGACTTAAAAGACCAAAGAGAGTCGAAGAG 2400 2402 CTATGCAACAGATCACAGAAAGACTTAAAAGACCACAAGAGAACTGGAGACTCTGGAG 2400 2403 CTATGCAACAGATCACAAGATTTAAAAGACCACCAAGAGTAAGGAACAGCTCTGGAG 2400 2404 CTATGCAACAGATCACAAGATTTAAAAGACCACCAAGAGTAAGGAACAGCTCTGGAG 2520 2461 CCCACCGAGTCCTACCTGAGGTGCCCTGGTAAAACTGAGGAAGATCTGCACCCTGGGC 2520 2521 CTCCAGCGCATCTTCTACCTGAAGCTGGAAACTGAGGAAGATCTGCACCTTGGAC 2580 2521 CTCCAGCGCATCTTCTACCTGAAGCTGGAAGATCTGCACCTTCCATCATTGAC 2580 [BAGCTCTTCCTGGACACCCTACTTTCTAATCAGGAGCAGTGGAGCAGTGAGCTGCCTCCTGCTCTTTTTTTT	2821 ATATTTAGGCATTGGGGGGGGGGGGGGTATAGTTCATGAGGGTTTTCTAAGA 2880 2881 AATTGCTAACAAAGACTTTTGGACAATGCTATCCCAGCAGAAAAAAAGGATAATA 2940 2881 AATTGCTAACAAAGACTTTTGGACAATGCTATCCAGCAGAAAAAAAA	3121 CTTCTTCCTTTATTTTAACAATGGTGAAAGATGGAGGATTACCTACAAATCAGACATGG 3180 3121 CTTCTTCCTTTATTTTAACAAATGGTGAAAGATGGAGGATTACCTACAAATCAGACATGG 3180 3181 CAAAACAATAATGGTTTGCTTCCTTAAACAAGTGCAATTTTTTAAAGTGCTGTCTTA 3240

1201 ACCAGGGCACTCCCCCGGCCCCCCCTCCCCCCTCCTCCTCCTCTCCTCC
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Sequence 78, Application US/09853386;
Batent No. US20020049151A1
GENERAL INFORMATION:
APPLICANT: Murphy, Evelyn
APPLICANT: Conneely, Orla
TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the 1;
TITLE OF INVENTION: Herapeutic Approaches to Diseases by Suppression of the 1;
TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors
FILE REFERENCE: P01972US1
CURRENT FAPLICATION WUMBER: US/09/853,386
CURRENT FILING DATE: 2001-05-11
PRIOR FILING DATE: 2000-05-12
PRIOR FILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 153
SOFTWARE: Patentin version 3.1
FEATURE PATENTIAL PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CACCCGCTCCCTCACTCGCACACACACACACGCGCCACAGGGCTCCG--CACACAC 178
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                                                                TATAGATATAATTTTAATTTTTGTTA--TTGGTTAAGGAGA-CAATTTTGGAGAGCAAGCA
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Best Local Similarity 99.4°
Matches 3779; Conservative
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CRGANISM: HUMAN
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                                                                            AGCCCACCGAGTCCTGGGTGCCCTGGTAGAACTGAGGAAGATCTGCCACCCTGG
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23) GEOGRAPHICA CONCENTE CONTROLLED AND CONTROLLED		1379 CCGCTGCCGCTCAGCCTGCCGCTGGGAGCCGCCGCGGGGGCGGCCAGCCA	1439 CGCTTGAGAGCCACCCGTACGGGCTGCCGCTGGCCAAGAGGGCCGCCGCTGGCCTTCC 1498	155 156	161		1679 AGAGAACAGTGCAGAAAATGCAAAATTTGCTTGCCAGCAATAAAAACTGCCCAGTAG 1738 	ACAAGAGACGTCGAAACCGATGTCAGTACTGTCGATTTCAGAAGTGTCTCAGTGTTGGAA 179	1799 TGGTAAAAGAAGTTGTCCGTACAGATAGTCTGAAAGGGAGAGAGA		1919 GCATGATGACCCTTGTCCGAGCTTTAACAGACTCAACACCCAGAGATCTTGATTATT 1978 		2039 TCTACAACCTCCTGACAGCCTCCATTGATGTATCCAGAAGCTGGGCAGAAAAGATTCCGG 2098 [2099 GATTTACTGATCTCCCCAAAGAAGATCAGACATTACTTATTGAATCAGCCTTTTTGGAGC 2158 [TGTTIGICCTCAGACTTICCATCAGGTCAAACACTGCTGAAGAIAAGTTTGTGTTGTG		2279 TTAAAGACTTTTCCTTAAATTTGCAGAGCCTGAACCTTGATATCCAAGCCTTAGCCTGCC 2338	2339 IGTCAGCACTGAGCATGATCACAGAAAGACATGGGTTAAAAGAACCAAAGAGAGTCGAAG 2398 	2399 AGCTATGCAACAAGATCACAAGCAGTTTAAAAGACCACCAGAGTAAGGGACAGGCTCTGG 2458
CGCCGAACTGGAACGCCCCTCCCGGGGTTCATTTGCAACGCTGACGGGGGGGG	අ <u>ග</u> 	S S	& A	ò a	<i>ò</i> €	<i>ò</i> €	yo a	δ da	· 영	yo da	yo da	λό dd	₩ 6	λό da	yo da	δ a	& g	ζς dd	۸۵
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                                                          AACATGCAAATCAGCAGGAACTGGTCATACAGGGTAAGCACCCAGGACAATAAGGATTTT
                                                                        3601- AACATGCAAATCAGCAGGAACTGGTCATACAGGGTAAGCACCAGGGACAATAAAGGATTTT
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; Sequence 1, Application US/202028841
; CENERAL INFORMATION:
; APPLICANT: MULLICAN, SHANNON E.
; APPLICANT: CONNEELY, ORLA M.
; APPLICANT: MILBRANDT, JEFFREY
; TITLE OF INVENTION: NOR-1 AND NUR77 NUCLEAR RECEPTORS AS TARGETS FOR
; TITLE OF INVENTION: ANT-LEUKEMIA THERAPY
; FILE REFERENCE: P02454US1
; CURRENT APPLICATION NUMBER: US/10/414,080
; CURRENT FILING DATE: 2003-04-15
; PRIOR PLILING DATE: 2002-04-17
; PRIOR FILING DATE: 2002-04-17
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Best Local Similarity 99.4%; Pred. No. 0;
Matches 3779; Conservative 0; Mismatches
                                                                                                                                                                                                    3773 GAGTGTGAGTACTAGGAAGGAT 3794
                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO
LENGTH: 3802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-414-080-1
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AGCTATGCAACAAGATCACAAGCAGTTTAAAAGACCACCAGAGTAAGGGACAGGCTCTGG
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APPLICANT: Zhong et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOP
FILE REFERENCE: 21402-608
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CURRENT FILING DATE: 2003-09-09

PRIOR PILING DATE: 2003-09-09

PRIOR PILING DATE: 2001-09-09

PRIOR PILING DATE: 2001-06-04

PRIOR FILING DATE: 2001-06-04

PRIOR PILING DATE: 2001-06-06

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PRIOR PLING DATE: 2001-06-11

PRIOR PLING DATE: 2001-06-12

PRIOR PLING DATE: 2001-06-12

PRIOR PLING DATE: 2001-06-14

PRIOR PLING DATE: 2001-06-15

PRIOR PLING DATE: 2001-06-16

PRIOR PLING DATE: 2001-06-21

                                                   3661 TATAGATATATATTTTTGGTAATTTTTGGGGGTTAAGGAGACCAATTTTGGAGGAGACA
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98.1%; Score 3722; D

Best Local Similarity 99.4%; Pred. No. 0;

Matches 3779; Conservative 0; Mismatches
                                                                                                                                                                                                                                                          GAGTGTGAGTACTAGGAAGGAT 3794
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 115, Application US/10659004 Publication No. US20050048507A1 GENERAL INFORMATION:
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US-10-659-004-115
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ORGANISM: Homo
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3061 AIGCTTCCTGTATCAAAGGTACGTATGTGGTGCAAACAAGGCAGAAACTTCCTTTTAATT 3120
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3541 TGACTGGTATATTCATTCAGAAGCGCCATAAGTCAGTTGAGTATTTGATCCCTAGATAAG
                                                                                                     3601 AACATGCAAATCAGCAGGAACTGGTCATACAGGGTAAGGACACCAGGACAATAAGGATTT
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                                           TGACTGGTATATTCATTCAGAAGCGCCATAAGTCAGTTGAGTATTTGATCCCTAGATAAG
                                                                                          AACATGCAAATCAGCAGGAACTGGTCATACAGGGTAAGGCACCAGGGACAATAAGGATTTT
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OTHER INFORMATION: Incyte ID No. US20030194721A1 349343.3
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                                                                                                                                                                                                                                                                                          Sequence 105, Application US/10247671
; Sequence 105, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiffman, Dov.
; APPLICANT: SASET, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAN
; FILE REFERENCE: PA-0050 US
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/323,784
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL PROGram
; SEQ ID NO 105
; LENGTH: 5828
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98.1%; Pred. No. 0;
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LOCATION: 1012-1074, 4044-4074, 5807

SOTHER INFORMATION: a, t, c, g, or other

US-10-247-671-105
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Best Local Similarity 98.1:
Matches 3728; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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US-10-247-671-105
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                                                                   2461 AACCCAACGAGTCCAAGGTCCTGGTTGCCCTGGTAGAACTGAGGAAGATCTGCACCCTGG
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239 GEGCCGAGGTTGGACCCCTCCCCGGGCTCACTTTTGCAACCCTGAGCCGGGCTGGTCCCCGGGCGGG

Qy 3536 AACTGACTGGTATATTCATTCAGAAGCGCCATAAGTCAGTTGAGTATTTGATCCCTAGAT 3595 bb 3541 AACTGACTGGTATATTCATTCAGAAGCGCCATAAGTCAGTTGAGTATTTGATT 3600 Qy 3596 AAGAACATGCAAATCAGCAGGAACTGGTCATACAGGGTAAGCACCAGGGACAATAAGGAT 3600 Db 3601 AAGAACATGCAAATCAGCAGGAACTGGTCATACAGGGTAAGCACCAATAAGGAT 3600 Qy 3656 TTTTATAGATATTTATTTTTTTTTTTTTAAGGAGACAATTTTGGAGAGCAATAAGGATTTTAGAAAAATATTTTTTTT	C-229 9, Application US/09873367C No. US20030165839A1 No. US20030165839A1 No. US20030165839A1 Young, Paul Soppet, Daniel Endress, Gregory Augustus, Meena Ebner, Reinhard Carter, Renneth	Query Match 75.8%; Score 2875; DB 10; Length 4977; Best Local Similarity 98.1%; Pred. No. 0; Manatches 19; Gaps 9; Matches 3008; Conservative 0; Mismatches 40; Indels 19; Gaps 9; Qy 733 CCTGGGGCCAATATAGCCCTTCCCCTCCAGGTTATGCGGCGCAG 790
2401 AAGAGCTATGCAACAAGCAGTTTAAAAGACCACCAGAGTAAGGGACAGGCTC 2460 2456 TGGAGCCCACCGAGGTCCTGGGTGCCTGGTAGAACTGAGGACATCTGCACCC 2515 [CTGGCTCTTTTCCTTACAACCTAAAGCCAGAAACTTGCAGGTATTGTGTTGGGGTTGT CTGGCTCTTTTCCTTACAACCTAAAGCCAGAAAACTTGCAGGAGTATTGTGTTGGGGGTTGT CTGGCTCTTTTCCTTACAACCTAAAGCCAGAAAACTTGCAGGAGTATTGTGTTGGGGGTTTTC GTTTTATATTTTAGGCATTGGGGGATGGGGAGGGGGTTATGTTCATGAGGGTTTTTC TAAGAAATTTTAGGCATTGGGGGATGGGGAGGGGGTTATCCTAGGGGGTTTTTTTT	3236 TCTTACTAGTTATTAACTCTCTTTATTCTATTGGAATAAAAAGGGGCAG 3295 3241 TCTTACTAAGTCTTGTTTATTAACTCTCTTTATTGGAATAAAAAGGGGCAG 3295 3241 TCTTACTAAGTCTTGTTTAATTAACTCTCTTTATTGGAAATAAAAGGAGGCAG 3206 TCATGTTAGCAAATGACACTTAATACTCCTAGCAGAGGCTGTGTTCACCTTCCCTGTCG 3350 3301 TCATGTTAGCAAATGACACGTTAATATCCCTAGCAGAGGCTGTGTTCACCTTCCCTGTCG 3360 3356 ATCCCTTCTGAGGAAATGACACTTATAGGCCATTCTTGATGGAACCAGATCC 3415

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791 CATACAGCTCGGAATACACCACGGAGATCATGAACCCCGACTACACAAGCTGACCATGG 850
154 CATACAGCTCGGAATACACCACGGAGATCATGAACCCCGACTACACACAAGCTGACATGG 213
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Sequence 63, Application US/10755889

Publication No. US20040171823A1

GENERAL INFORMATION:

APPLICANT: BISECOL-Mers Squibb Company

TITLE OF INVENTION: PATHWAY

PILE REPERENCE: DO284 NP

CURRENT FILING DATE: 2004-01-13

PRIOR FILING DATE: 2004-01-14

PRIOR FILING DATE: 2003-01-14

PRIOR FILING DATE: 2003-01-14

PRIOR FILING DATE: 2003-05-12

NUMBER OF SEQ ID NOS: 823

SOFTWARE: Patentin version 3.2

SEQ ID NO 63

LENTH: 4977
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ATGGCTGTTTGCTTCCATAAACAAGTGCAATTTTTTAAAGTGCTGTCTTACTAAGTCTTTG
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	811 TIGICCGTACAGATAGICTGAAAGGAGAGAGGTCGTCTGCCTTCCAAACCAAA	4 TIGICCETACAGATAGICTGAAAGGGAGGAGGCTCTCTGCCTTCCAAACCAAA	4 CATTACAGAGAACCTTCTCAGCCCTCTCCACCTTCTCCTCCAATCTGCATGATGATG 1 CCCTTGTCCGAGCTTTAACAGACTCAACACCCCAGAGATCTTGATTATTCCAGATACTGTC 1	CTCTTGTCCGAGCTTTAACAGACTCAACACCCAGAGATCTTGATTATTCCAGATACTGTC CCACTGACCAGGCTGCTGGGGACAGATGCTGACATGTGCAACAACAATTCTACAACCTCC ACACTGACCAGGAACAACAATCTGCAAGCATGTGCAAGCATGTGCAAGCATGTTGCAAGCATGTTGCAAACAATTCTACAACACTCCAACAACAATATCTACAACA	TGACAGCCTCCATTGATGTACCAGAAGCTGGCCAGAAAGGATTCCGGGATTTACTGATCTCAGACTTCCGGGATTTACTGATCTCAGATCCGGCATTACTGATCTCAGATCTCCGGGATTTACTGATCACTCCAGAAAGGTGGGCCAGAAAAGATTCCGGGATTTACTGATCCAGAAAGGTGGGCCAGAAAAGATTCCGGGGATTTACTGATCCAGAAAAGGATACCGGGATTACTGATC	TCCCCAAAGAAGATCAGACATTACTTATTGAATCAGCCTTTTTGGAGCTGTTTGFCCTCA 	GACTITICCATCAGGICAAACACIGCIGAAGAIAAGITIQIGITICIGCAATGGACTIGICC 	IGCALCGACTICAGIGCCTICGIGGATITGGGGGAGIGGCTCGACTCTATIAAAGACTTTT 	CCTTAAATTTGCAGAGCCTGAACCTTGATATCCAAGCCTTAGCCTGCCT	GCATGATCACAGAAAGACATGGGTTAAAAGAACCAAAGAGGGGCGGAAGAGCTATGCAACA 	agatcacaaggagtttaaagaccaccagagtaaggaacaggctctggagcccaccgagt 	CCAAGGTCCTGGGTGCCCTGGTAGAACTGAGGAAGATCTGCACCCTGGGCCTCCAGCGCAACAAAAAAAA	1 TCTTCTACCTGAAGCTGGAAGACTTGGTGTCTCCACCTTCCATCATTGACAAGCTCTTCC	TGGACACCCTACCTTTCTAATCAGGAGCAGTGGAGCAGTGAGCTGCCTCCTCTCCTAGCA 	CCTGCTTGCTACGCAGCAAAGGATAGGTTTGGAAACCTATCATTTCCTGTCCTTCTTA	agaggaaaagcagctcctgtagaaagcaaagactttcttt	acaacctaaagccagaaacttccagagtattgtgttggggttgtgtttatatttaggc 	ATTGGGGGATGGGGGGGTTATAGTTCATGAGGGTTTTCTAAGAAATTGCTAACIN

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                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORREATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION NUMBER: <UNKnown>
PRIOR APPLICATION NUMBER: <UNKnown>
APPLICATION NUMBER: <UNKnown>
ATTORNEY AGENT INFORMATION:
ANNEY: ZAIL NEVERATION:
ANNEY: ZAIL NEVERATION:
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                         NUMBER OF SEQUENCES: 1508
CORRESSPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALLFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 70.9%; Score 2689.6; Best Local Similarity 99.9%; Pred. No. 0; Matches 2692; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 1
TELECOMMUNICATION INFORMATION:
TELEFAN: (650) 855-0555
INFORMATION FOR SEQ ID NO: 928:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; CLONE: 91311564
; SEQUENCE DESCRIPTION: SEQ ID NO: 928
US-10-641-643-928
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TITLE OF INVENTION:
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APPLICANT: Murphy, Evelyn
APPLICANT: Bresnihan, Barry
APPLICANT: Conneely, Orla
APPLICANT: Fitzgerald, Oliver
APPLICANT: Fitzgerald, Oliver
TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors
FILE REFERENCE: P01972013
FILE REFERENCE: P01972013
FURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/203645
PRIOR PLILING DATE: 2000-05-12
PRIOR PLILING DATE: 2000-05-13
SOFTWARE: Patentin version 3.1
SEQ ID NO 4.70
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Best Local Similarity 83.4%; Pred. No. 0;
Matches 3131; Conservative 0; Mismatches 535; Indels
                                                                                Sequence 47, Application US/09853386; Patent No. US20020049151A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                TYPE: DNA ORGANISM: Rattus norvegicus
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                                                                   RESULT 11
US-09-853-386-47
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GENERAL INPORMATION:
APPLICANT: Guenther, Catherine
APPLICANT: Allen, Reith D.
TITLE OF INVENTION: TRANSGENIC MICE CONTAINING NOR
TITLE OF INVENTION: DISRUPTIONS
FILE REPERENCE: RE-687
CURRENT APPLICATION NUMBER: US 60/251, 794
PRIOR APPLICATION NUMBER: US 60/251, 794
PRIOR FILING DATE: 2000-12-06
PRIOR FILING DATE: 2000-12-06
PRIOR FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FASLESC for Windows Version 4.0
SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION OF SECUENCE AND ADDITION
                                                                                                                                                                                                                                                                                                                                                          Score 2500;
Pred. No. 0;
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Best Local Similarity 83.4%;
Matches 3131; Conservative 0
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; ORGANISM: ratus norvegius
US-10-005-169-3
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2752 TAAAGCCAGAAAACCTTGCAGAGTATTGTGTTGGGGTTGTTTTATATTTAGGCTTTTGGT
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                                                                              GGATGGGGTGGGAGGGT--TATAGTTCATGAGGGTTTTCTAAGAAATTGCTAACAAAG
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RESULT 12 US-10-005-169-3 Sequence 3, Application US/10005169 ; Publication No. US20020152492A1

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ر م	870 CACGGCTACAGCCACACGTCCCTGCCCAGCATCAGTACCTTCGTGGAGGCTACTCGAG 929 	à a	CCGAGCTITAACAGACCCAGAGATCITGATTATTCCAGATACTGCCAGTGA 1997 CCGAGCTTTAACAGACGCCCAGAGACCTTGATTACTCCAGATACTGCCCACCGA 197
<u>ک</u> ۾	930 CAACTACGAACTCAAGCCTTCCTGCGTGTACCAATGCAGCGGCCCTT 977 	ò 8	1998 CCAGGCTGCTGCAGGCACAGATGCTGAGCATGTGCAACAATTCTACAACCTCCTGACAGC 2057
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8 6 B	CCACCACCACCATCACCAGCAGCAGCATCAGAGCCATCCAT	ሯ	2118 AGAAGATCAGACATTACTTATTGAATCAGCCTTTTTGGAGCTGTTTGTCCTCAGACTTTC 2177 2094. AGAAGATCAGACGTTATTAGAATCAGCCTTTTTTGGAGCTGTTCGTTC
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                                           AAGGGTTG-TTCGCCAGGGTAGGATGTCTTAAAGATTGGTCCCTTGAAAATATGCTTC
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US-10-414-080-2
; Sequence 2, Application US/10414080
; Sequence 2, Application US/10414080
; Publication No. US20030220288A1
; GENERAL INFORMATION:
; APPLICANT: MULLICAN, SHANNON E.
; APPLICANT: CONNELLY, ORLA M.
; APPLICANT: CONNELLY, ORLA M.
; TITLE OF INVENTION: ANTI-LEUKEMIA THERAPY
; TITLE OF INVENTION: ANTI-LEUKEMIA THERAPY
; FILE REFERENCE: PO2454USI
; CURRENT APPLICATION NUMBER: US/10/414,080
; CURRENT FILING DATE: 2003-04-15
; PRIOR PILING DATE: 2002-04-17
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                                                                               Length
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                                                                             Score 2500; DB 17;
Pred. No. 0;
0; Mismatches 535;
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Best Local Similarity 83.4%;
Matches 3131; Conservative 0
) NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patentin Ver. 2
; SEQ ID NO 2
; LENGTH: 4400
; TYPE: DNA
; ORGANISM: RAT
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                                                                                               AGTCATGTTAGCAAATGACACGTTAATATCCCTAGCAGAGGCTGTGTTCACCTTTCCCTGT
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Sequence 209, Application US/10191803

Sublication No. US20040014040A1

Sublication No. US2004014040A1

Sublication No. US2004014040A1

Subrication No. US2004014040A1

Subricant: Menchick Mark

APPLICANT: PORTER, Mark

APPLICANT: HIGGS, Brandon

APPLICANT: HIGGS, Brandon

APPLICANT: GASTLE, Arthur

APPLICANT: GASTLE, Arthur

APPLICANT: GASTLE, Michael

FILE REFERENCE: 44921-5690US

CURRENT PILING DATE: 2002-00-10

PRIOR FILING DATE: 2001-07-10

PRIOR FILING DATE: 2001-07-17

PRIOR PLING DATE: 2001-07-17

PRIOR PRICATION NUMBER: US 60/305,623

PRIOR PRICATION NUMBER: US 60/305,611

PRIOR PRING DATE: 2002-04-03

PRIOR PRING DATE: 2002-05-06

NUMBER OF SEQ ID NOS: 1140

SOFTWARE: Patentin Ver: 2.1

SEQ ID NO 209

LENGTH: 4400
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                                  US20040014040A1 NM_031628
                                                                                               90;
                                                                      Length 4400;
                                                                                               Indels
                                                                   Score 2500; DB 17;
Pred. No. 0;
0; Mismatches 535;
; TYPE: DNA; ORGANISM: Rattus norvegicus; FATUNE:; OTHER INFORMATION: Genbank Accession No. US-10-191-803-209
                                                                       Query Match
Best Local Similarity 83.4%;
Matches 3131; Conservative
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2058 CTCCATTGATGATGTATCCAGAAGCTGGGCAGAAAAGATTCGGGGATTTACTGATCTCCCCCAA 2117 2034 CTCCATTGATGTCCAGAAGCTGGGCAGAAAGATTCCGGGGATTTACTGATCTCCCCCAA 2093 2118 AGAAGATCAGACATTACTTATTGAATCAGCCTTTTTGGAGCTGTTTGTCCTCCAGACTTTC 2177 2094 AGAAGATCAGACATTACTTATTGAATCAGCCTTTTTTGGAGCTGTTTCTTTTTGAGCTTTTCTCTTAGACTTTC 2153 2178 CATCAGGTCAAACACTGCTGAAGAATAGGTTTTTTTTTT	2214 ACTTCAGTGCCTTCGCGGATTTGCGAGTGGCTCGACTCCATTAAAGACTTTTCTTTAAA 2273 2298 TTTGCAGAGCCTGAACCTTGATATCCAAGCCTTAGCCTGCTGCTCAGCACTGAGCATGAT 2357 2274 TTTGCAGAGCCTGAACCTTGATATCCAAGCCTTAGCCTGCCT		2478 CCTGGGGTGCCCTGGTAGAACTGAGGATCTGCCCTGGGCCTCCGCATCTTTA 2537 2454 CCTTCGCGCACTGGTGCAACTGAGGAAGATCTGCACGCCTCCAGGCCTCCAGCGTATCTTCTA 2513 2538 CCTGAAGCTGGAAGACTTGGTGTCTCCACCTTCCATCATGACAAGCTCTTCCTGGACAC 2597 2514 CCTGAAGCTGGAAGACTTGGTGTCCCCACCTTCCATCATGACAAGCTCTTCCTGGACAC 2597 2514 CCTGAAGCTGGAGGACTTGGTGTCCCCACCTTCTGTCACAAGCTCTTCCTGATAC 2573	2598 CCTACCTTTCTAATCAGGAGCAG-TGGAGCAGGAGCTGCCTCCTCCTAGCACCTGCT 2656	2717 AAAGCAGCTCCTGTAGAAAGCAAAGACTTTCTTTTTTTCTGGCTCTTTTCCTTACAACC 2776 [2837 GGATGGGGGGGGGGG-TATAGTTCATGAGGGTTTTCTAAGAAATTGCTAACAAAG 2894	CACTTITIGGATCATGCTATCCCAGCAGTGGGGAGAAAGGATAATATAACTGTTTT AAAACTCTTTCTGGGGGAATCCAATTATAGTTGCTTTGTATTTAAAAACAAGACGCC	3007 AAGGGTTG-TTCGCCAGGGTGGTCTTAAAGATTGGTCCTTGAAATTGGTTC 3065
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978 GATCAAAGTGGAGGGGGGGGCCCAGCTACCATCACCACCACCACCACCACCACCACCACCACCAC	TCTGC ACGGT CCAAT	1278 GGCCGCGCGCGTTCCCGCTCTTCCACTTCAAGCCCTCGCCGCATCCCCCCGGCCC 1337	1398 GCGCTGGGAGCCGCAGCCGCGGGAGCCAGGCCGCCGCTTGAGAGCCACCCGTA 1457	CCCCTACCGGTTGGCCTGCTGGGCGAGAGTCCCAGCCGTCCGGTTGGGCCTCCACAGCTGGCGCGCGC	CTACGGGAACCTGCGAGGGCTCCAGGGCTTTTCAAGAGAACGTGCGGGGAAAAACTACCAGGGAGAAAAAAAA	1674 CGCAAAATATGTTTGCCAAATAAAAACTGCCCGGTAGACAAGAGACGTCGAAATCG 1733 1758 ATGTCAGTACTGTCGATTTCAGAAGTGTCTCAGTGTTGGAATGGTAAAAAAAGTTGTCCG 1817 1734 ATGTCAGTACTGCAGGTTTCAGAAGTGTCTCAGTGTCGGGATGGTGAAGGAAG		1918 CCGAGCTTTAACAGACTCAACACCCAGAGATCTTGATTATTCCAGATACTGTCCCACTGA 1997

CATTCTTCTTCTTTAAATAAATAAATAAAAAAAAAAAA
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221 ITTCCTTACAMCCTAMAGCCGANACTTGCAGGTATTGTGTGGGGTTGTTTTATACATTCTACAGGTATTGTTGTGGGGTTTGTTT
B & B & B & B & B & B & B & B & B & B &
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1081 CGCACCTCCGACGCCTCCAAACACCCCCGTAAACACCCCGAAAACACCCCCAAACCCAAACACCCCTCCCAAACCCCCCTCCCAAACACCCCCTCCCAAACCCCCC

Search completed: March 22, 2005, 01:21:50 Job time : 2024 secs

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Query Match
Best Local Similarity 94.9
Matches 919; Conservative
Bos sp.
Bos sp.
                            461.6
4422.2
429.4
428.8
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COMMENT
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BK925243 BK925243
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                            Compugen Ltd.
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             GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compug
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Match Length DB
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3794
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9b_est3:;
9b_est4::
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Roslin Institute
Roslin, Midlothian, EH25 9PS, UNITED KINGDOM
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Bases called and trimmed with phred
OS 20425.c. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options Vector:pBluescriptII(SK+) R. Site
1:ECGRV(lost) R. Site 2:NotI Seq Primer: T7 Normalised library
constructed from pooled monocytes from Bos taurus (Holstein) and
Bos indicus (Sahiwals) cattle subjected to various stimuli,
including infection with the protozoan parasite Theileria annulata.
Location/Qualifiers
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/cell_type="bovine monocyte"
/clone_lib="KN206"
/clone_lib="KN206"
/othore="Vector: pBluescriptII(SK+); Site_1: EcoRV(lost);
Site_2: Not!; Normalised library constructed from pooled monocytes from Bos taurus (Holstein) and Bos indicus (Sahiwals) cattle subjected to various stimuli, including infection with the protozoan parasite Theileria annulata"
                                          BF604409 270232 MA
CR548239 DKZ24559N
M40449 yx89cC6.rl
A1911009 wd23c12.x
BG239565 maf19h02.
AY417754 Pen trogl
BB758614 BB758614
BF019466 ux10e11.y
AW49389 UI-M-BH3-
AV645902 AV645408
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BG32641 UI-M-BH2.
BG32641 CM2-CN006
CK559326 UII-leng
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
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AJ814207 KN206 Bos sp. cDNA clone C0005204p19, mRNA sequence.
AJ814207
AJ814207.1 GI:51881683
                        AK087495
BF604409
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1 (bases 1 to 996)
McGuire,K. and Glass,E.J.
Unpublished ESTs, McGuire and Glass
Unpublished (2004)
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/organism="Bos sp."
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AI145834
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BMS57376 1087 bp mRNA linear EST 20-FEB-2002 AGENCOURT_6561893 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5547838

3048 3228 3108 480 300 TTAAAAACAAGAACAGCCCAAGGGTTCTTCGCCAGGGTAGGATGTGTCTTAAAAGATTGGTC 180 /organism="Homo sapiens"
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E 1 (bases 1 to 1087)

E NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.llnl.gov

Plate: LLAM12255 row: m column: 23

High quality sequence stop: 624. Euteleostomi; 421 GAGGCAGTCATGTTAGCAAATGACACGTTAATATCCCTAGCAGAGGCTGTGTTCACCTTC CCTTGAAAATATGCTTCCTGTATCAAAGGTACGTATGTGGTGCAAACAAGCAGAAACTT CCTTTTAATTTCCTTCTTCCTTTATTTTAACAAATGGTGAAAGATGGAGGATTACCTACA AATCAGACATGGCAAAACAATAATGGCTGTTTGCTTCCATAAACAAGTGCAATTTTTAA GAGGCAGTCATGTTAGCAAATGACACGTTAATATCCCTAGCAGAGGCTGTGTTCACCTTC 241 CCTTTTAATTTCCTTCTTCTTTTTAACAATGGTGAAAGATGGAGGATTACCTACA TTAAAAACAAGAACAGCCAAGGGTTGTTCGCCAGGGTAGGATGTGTCTTAAAAGATTGGGTC 181 CCTTGAAATATGCTTCCTGTATCAAAGGTACGTATGTGGTGCAAACAAGGCAGAAACTT GGTTTTCTAAGAAATTGCTAACAAAGCACTTTTGGACAATGCTATCCCAGCAGGAAAAAA GGTTTTCTAAGAAATTGCTAACAAAGCACTTTTGGACAATGCTATCCCAGCAGGAAAAA Gaps 10; Length 1087; Query Match 21.0%; Score 796; DB 4; Length 10 Best Local Similarity 96.7%; Pred. No. 3.3e-182; Matches 878; Conservative 0; Mismatches 20; Indels Homo sapiens (human) 3289 à

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E. (Bases I to 1032)

S. NIH-MCC http://mgo.nci.nih.gov/.

I. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop; 651.
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/ organism="Homo sapiens"
/ db_xref="mRNA"
/ db_xref="taxon:9606"
/ clone="INAGE:5745831"
/ lab host="DH108"
/ lab host="DH108"
/ clone lib="NHH MGC 118"
/ lone lib="NHH MGC 118"
/ lone setroyed); RNA source leukcytes from anonymous poonon-activated adult donors. Library is oligo-dT pri
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and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb, insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     425 AGCCAGAAAACTTGCAGAGTATTGTGTTGGGGTTGTGTTTTATATTTTAGGCATTGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               725 GTATGTGGCGCAAAACAACGCAGAAACTTCCTTTTAATTTCCCTCTTCCCTATTTACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2360 CAGAAAGACATGGGTTAAAAGAACCAAAGAGTCGAAGAGCTATGCAACAAGATCACAA
                                                                                                                                                                                                                                                                                 CCGGAATTCCTCGGGATAAAGAACCAAAGAGAGTCGAAGAGCTATGCAACAACAACAAA
                                                                                                                                                                                                                                                                                                                                         GCAGTTTAAAAAGACCACCAGAGTAAAGGGACAGGCTCTGGAGCCCACCGAGTCCAAGGTCC
                                                                                                                                                                                                                                                                                                                                                                  65 GCAGTTTAAAAGACCACCACCAGAGTAAGGGACAGGCTCTGGAGCCCACCGAGGTCCAAGGTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2600 TACCTITCIAAICAGGAGCAGTGGAGCAGTGAGCTGCCTCCTCCTAGCACCTGCTTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            485 TGGGGGGGGGGGTTATAGTTCATGAGGGTTTTCTAAGAAATTGCTAACAAAGCACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2900 TTGGACAATGCTATCCCAGCAGAAAAAAAAGGATAATATAACTGTTTTAAAACTCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             545 TIGGACAATGCTAICCCAGCAGGAAAAAAAAGGATAATATAAACIGTITIAAAAACTCTTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2960 TGGGGAATCCAATTATAGTTGCTTTGTATTTAAAAACAAGAACAGGCTTGTTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAATGGTGAAAGATGGAGGATTACCTACAAATCAGACATGGCAAAACAATAATGGCTG--
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                                                                                                                                                                   Length 1032;
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                                                                                                                                                                   Score 769.4; DB 4;
Pred. No. 9.7e-176;
0; Mismatches 46;
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Best Local Similarity 94.4%;
Matches 820; Conservative
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3405 GAACCAGATCCCTGCCCTGACTGTCCAGCTATCCTGAAAGTGGATCAGATTATAAACTGG 3464
                                                                                                                                                                                                                                                         3465 ATTACATGTAACTGTTTTGGTTGTGTTCTATCAACCCCACCAGAGTTCCCTAAACTTGCT 3524
                                                                                                                                                                                                                                                                                                                                                 3525 TCAGTTATAGTAACTGACTGGTATATTCATTCAGAAGCGCCATAAGTCAGTTGAGTATT 3584
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/note="Vector: pCMV SPORT6; Site 1: Not1; Site 2: Sal1;
Library made from pooled tissue from marrow, alveolar
macrophage, ovary, fetal semitendonosus muscle, and fetal
longissimus muscle."
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                       1 (bases 1 to 852)
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.
Smith, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.
Gasas, E., Wray, J.B., White, J., Cho, J., Fabrenkrug, S.C.,
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,
Chitko-McKown, C.G., Pertea, G., Holt, I., Karamycheva, S., Liang, F.,
Ohackenbush, J. and Keele, J.W.
Sequence evaluation of four pooled-tissue normalized bovine cDNA
libraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
single pass sequencing. Bases called with pred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified v
cross_match v0.990329.
Plate: 51 row. 1 column: 19
Seq primer: GTAATACGACTCACTATAGGG.
Location/Qualifiers
                                                                                                                                                                                               3345 CTTCCCTGTCGATCCCTTCTGAGGTATGGCCCATCCAAGACTTTTAGGCCATTCTTGATG
3285 AAAGGAGGCAGTCATGTTAGCAAATGACACGTTAATATCCCTAGCAGAGGCTGTGTTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CK778210 852 bp mRNA linear 965365 MARC 3BOV Bos taurus CDNA 3', mRNA sequence. CK778210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4360
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                         3585 GATCCCTAGATAAGAACATGCAAATCAGCAGGAA 3618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       721 GATCCCTAGATAAGAACATGCAAATCAGCAGGA 754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Bos taurus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9913"
/tissue_type="pooled"
/lab_host="DH108"
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CK778210/c
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I. (Dasses 1 to 819)

NIH-MGC http://mgc.nci.nih.gov/.

L. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov/
Tissue procurement: ATCC/DCTD/DTP

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Location/Qualifiers

High quality sequence stop: 694.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:619660"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NHH MGC 72"
/note="Organ: 8Kin; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies."
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                         BQ431513 819 NH_MGC_72 Homo sapiens cDNA clone IMAGE:6159660 5', mRNA Sequence.
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0
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Best Local Similarity 99.9%; Pred. No. 1.3e-171;
Matches 753; Conservative 0; Mismatches 1; Indels 0
                                                                                                   BQ431513
BQ431513.1 GI:21170589
                                                                                                                                                               Homo sapiens (human)
Homo sapiens
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E DOUISE TO 671)
SSmith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.
Waray, J.E. and Keele, J.W.
A second set of bovine ESTS from pooled-tissue normalized libraries Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4360
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with plate: FQX8053 row: I column: 18
Seq primer: GTANTACAGACTAGTAGGG.
                                 Chordata; Craniata; Vertebrata; Euteleostomi; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 CCGTACAGACAGTCTGAAAGGGAGAAGAGTCGGCTGCCTTCCAAACCAAAGAGCCCATT
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                                                                                                                                                                                                                                                                                                                                                                                 /.organism="Bos taurus"
/mol_type="mRNA"
/db xref="taxon:9913"
/lab lot="type="pooled"
/lab host="DH108"
/clone_lib="WARC 6BOV"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
linclary made with RNA pooled From multiple tIssues
lincluding liver, lung, hypothalamus, pitultary, and
placenta/endometrium."
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Pred. No. 2.6e-141;
0; Mismatches 27;
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                               Eukaryota; Metazoa;
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Bovinae; Bos.
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Matches 644; Conserv
 Bos taurus
Bos taurus
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                                                                              CTGGGCAGAAAAGATTCCGGGATTTACTGATCTCCCCAAAGAAGATCAGACATTACTTAT
                                                                                                                                                                  789 AGAATCAGCCTTTTTGGAGCTGTTTGTTCTCAGACTTTCCATCAGGTCAAACACTGCTGA
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                                                                                                   CGGGGCAGAAAAGATTCCCGGATTTACTGATCTCCCCAAAGAAGATCAGAAGATTACTTAT
                                                                                                                                                                                                                  AGATAAGTTTGTGTTCTGCAATGGACTTGTCCTGCATCGACTTCAGTGCCTTCGTGGATT
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                 Length 852;
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                                               Indels
              Score 696.4; DB 7;
Pred. No. 5.5e-158;
0; Mismatches 56;
              Query Match
Best Local Similarity 92.6%;
Matches 787; Conservative
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/ organism="Momo sapiens"
// mol_type="mRNA"
// db_xref="taxon:9606"
// clone="MNAE:1049856"
// tissue_type="monose"
// tissue_type="pooled"
// lab host="DH10B (T1 phage-resistant)"
// clone=lib="NIH MGC 191"
// clone=lib="WIH MGC 191"
// clone=lib="NIH MGC 191"
// clone=lib="WIH MGC 191"
// site 2: Sil (agccattatggcc);
// and 3' adaptors were used in cloning as follows: 5' adaptor sequence:
s'-ATTCTACAGGCCGAGGGCGCGAATG-dT(30)BN-3' (where B = A, C, C, or G and N = A, C, G, or T). Average insert size 1.69
// cord and N = A, C, G, or T). Average insert size 1.69
// cord and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases I to 757)

IN IN-MGC http://mgc.nci.nlh.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Office of Cancer Genomics

Office of Cancer Genomics

National Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Narayan Bhat

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arraya Bhat

CDNA Library Arraya Bhat

CONA Library Arraya Bhy: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC.Clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

Http://image.llnl.gov

Http://image.llnl.gov

Http://image.llnl.gov

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                   CD521819
757 bp mRNA linear EST 06-JUN-2003 AGENCOURT 14360118 NIH_MGC_191 Homo sapiens cDNA clone iMAGE:30409856 5', mRNA sequence.
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481 TCGACTTCAGTGCCTTCGTGGATTTGGGGAGTGGCTCGACTCATTAAAGACTTTTCCTT 540
                                                                                                              2355 GATCACAGAAAGACATGGGTTAAAAGAACCAAAGAGAGTCGAAGAGCTATGCAACAAGAT
                                                                                                                                  Score 617; DB 6; Length 757;
Pred. No. 1.2e-138;
0; Mismatches 5; Indels
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Best Local Similarity 98.9%;
Matches 632; Conservative
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Homo sapiens (human)
Homo sapiens
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Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.990329.
Plate: LAMBODS row: F column: 20
Seq primer: GTAATACGACTATAGGG.
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2866 GAGGGTTTTCTAAGAAATTGCTAACAAGCACTTTTGGACAATGCTATCCCAGCAGGAAA
                              2926 AAAAAGGATAATATAAACTGTTTTAAAACTCTTTCTGGGGAATCCAATTATAGTTGCTTTG
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.

1 (bases 1 to 635)
Smith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keele, J.W.

A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                       with
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                                                                                                                                                                                                                                                                    Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /Lissue tree="pooled"
/lab_host="DH10B"
/clone lib="MARC 6BOV"
/note="Vector: pcDNA3.; Site 1: EcoRI; Site 2: NotI;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pitultary, and
placenta/endometrium."
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Pred. No. 7.3e-134;
0; Mismatches 24;
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Plate: FQY8056 row: B column: 15
Seg primer: GTAATACGACTCACTATAGGG.
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                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
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Best Local Similarity 96.2%;
Matches 611; Conservative
 EST.
Bos taurus (
Bos taurus
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                                                                                  /tissue_type="pooled"
/lab_host="pooled"
/lab_host="poll08"
/clone lib="MARC 6BOV"
/note="Vector: pcDNA3.1; Site_1: EcoR1; Site_2: Not1;
Library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."
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                      1. .679
/organism="Bos taurus"
/mol_type="mRNA"
/db_xref="taxon:9913"
Location/Qualifiers
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Gallus gallus
Gallus gallus
Gallus gallus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Aves; Neognathae; Galliformes; Phasianidae;
1 (bases I to 940)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Comprehensive Los), 1965-1969 (2002)
                                                                                                                    BU436288 100V-2002 940 bp mRNA linear EST 29-NOV-2002 603208116F1 CSEQREN11 Gallus gallus cDNA clone ChEST18303 5', mRNA
541 iditigitcicadactiticcarcandicaaacacidcidaagaraagirigigiicidca
                                                                                                                                                                                                                                                                                             Science and Technology
                                                          Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of
(UMIST)
PO Box 88, Manchester, M60 10D, UK
Tel: 01612008930
                                                                                                                                                                                                                                                                                                                                        Email: Simon. Hubbard@umist.ac.uk.
                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                BU436288
BU436288.1 GI:25925599
                                                                                                                                          sequence.
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                                                             2219
                                                                                                                                               ACCESSION
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 635)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   722 TAAGGTACTGGGTGTTCTTGCTG-ACTTGCGTCTCTGCGACTGGAGCGCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2187 AAACACTGCTGAAGATAAGTTTGTGTTCTGCAATGGACTTGTCCTGCATCGACTTCAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTGAACCTTGATATCCAAGCCTTAGCCTGCCTGTCAGCACTGAGATCACAGAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2427 AAAAGACCA------CCAGAGTAAGGGACAGGCTCTGGAGCCCACCGAGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACATTACTTATTGAATCAGCCTTTTTGGAGCTGTTTGTCCTCAGACTTTCCATCAGGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1887 ITCTCAGCCCTCCACCTTCTCCCAATCTGCATGAATGCCCCTTGTCCGAGCTTT
                                                                                                                                                                                 TTGGAGCCCTCCCGCCTTCTCCCATCAGCATGATGAACGCCCTCGTACGAGCTTT
                                                                                                                                                                                                                       1947 AACAGACTCAACACCCAGAGATCTTGATTATTCCAGATACTGTCCCACTGACCAGGCTGC
                                                                                                                                                                                                                                                242 IGCAGGCACAGATGCAGAACATGTACAACAGTTCTATAATCTTCTGACTGCCTCCATIGA
                                                                1827 TCTGAAAGGGAGGAGGAGGTCGTCTGCCTTCCAAACCAAAGAGCCCCATTACAACAGGAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGENCOURT 14534944 NIH MGC_191 Homo sapiens cDNA clone IMAGE:30417493 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGACACCCTACCTTTCTAA 2610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          841 GGACAACTITGCCTTCTGA 859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CD638747.1 GI:31804872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (human)
Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
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16;

15.4%; Score 583; DB 5; Length 940; 81.8%; Pred. No. 2.3e-130; Live 0; Mismatches 140; Indels

703; Conservative

Query Match Best Local Similarity Matches 703; Conserv

```
/tissue type="Pooled"
/lab_host="Invasion 133"/"
/lab_host="DA108 (T1 phage-resistant)"
/dlob_host="DA108 (T1 phage-resistant)"
/dlobe lib="NHH MGC 191"
/dlobe lib="NHH MGC 191"
/note="Vector: pDNR-LIB; Site_1: Sfil (ggccattatggcc);
Site_2: Sfil (ggccgcctcggcc); Library is oligo-dr primed and directionally cloned. PBMC - Peripheral Blood Mononuclear Cells. RNA was pooled from 3/6hour stimulation with PMA and nonowpoin. S' and 3' adaptor sequence:
5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGGCCCAGGCGCCATG-dT(30)BN-3' (where B = A, C, Or G and N = A, C, G, Or T). Average insert size 1.69
kb (range 0.70-5.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NITH-MGC http://mg.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Unpublished (1999)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Betheada, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayam Bhat
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llhi.gov
Rlate: NDCN208 row: e column: 02
High quality sequence stop: 483.
                                                                                                                                                                                                                                                                                                                                                                                             EST 06-JUN-2003
                                                                                                                                          483 GTTAAGGAGACAATTTTGGAGGGAAGCAAATCTTCTTTTTAAAAATAGTATGAATGTG 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 794)
                                       423 ACAGGGTAAGCACCAGGGACAATAAGGATTTTATAGATATAATTTAATTTTAGTTATTG
               3627 ACAGGGTAAGCACCAGGGACAAIAAGGAITTITAIAGATATAAITITAAITITIGITATITG
                                                                                                             3687 GTTAAGGAGACAATTTTGGAGAGCAAGCAAA---TCTTTTAAAAATAGTATGAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1768 IGTCGATTTCAGAAGTGTCTCAGTGTTGGAATGGTAAAAGAAGTTGTCCGTACAGATAGT
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                                                                                                                                                                                                                                                                                                                                                                   794 bp mRNA linear ES1
AGENCOURT 14356328 NIH MGC_191 Home sapiens cDNA clone
IMAGE:30413377 5', mRNA sequence.
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14.8%; Score 561; DB 6; Length 794;
Best Local Similarity 97.3%; Pred. No. 5.1e-125;
Matches 624; Conservative 0; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30413377"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CD522275.1 GI:31453993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3327 AGCAGAGGCTGTGTTCACCTTCCCTGTCGATCCCTTCTGAGGTATGGCCCATCCAAGACT 3386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTAGGCCATTCTTGATGGAACCAGATCCCTGCCCTGACTGTCCAGCTATCCTGAAAGTG 3446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 AGCAGAGGCTGTGTTCACCTTCCTGTGGATCCCTTCTGAGGTATGGCCCATCCAAGACT 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 TATTCTATATGGAAATAAAAGGGGGGGGCGTCATGTTAGCAAATGACACGTTAATATCCCT 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 TAAGTCAGTTGAGTATTTGATCCCTAGATAAGAACATGCAAATCAGCAGGAACTGGTCAT 422
NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

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Office of Cancer Genomics
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Bldg. 31 RM10A07 Betheda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Narayan Bhat
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayae Bhat
CDNA Library Arrayae by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDFM218 row: p column: 14
Hich minity accounts afron: 604
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                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 505.
Location/Qualifiers
1. .635
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                                 TITLE
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CK635592 802 bp mRNA linear EST 28-JAN-2004 UI-M-HNO-cnl-j-11-0-UI.rl NIH_BMAP_HNO Mus musculus CDNA clone IMAGE:30643330 5', mRNA sequence.
CK635592 GI:41361458
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                   2238 ACTICAGIGCCIICGIGGAITIGGGGAGIGGCICGACICIAITAAAGACIITICCIIAAA 2297
                                                                                                                                                                                                                                                                                                                                                                          CCTGGGTGCCCTGGAACTGAGGAAGATCTGCACCCTGGGCCTCCAGCGCATCTTCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCTGAAGCTGGAAGACTTGGTGTCTCCACCTTCCATCATTGACAAGCTCTTCCTGGACAC
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/tiseue_type="pooled"
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/clone_lib="MARC 6BOV"
/note="Vector: pcDNA3.1; Site_1: EcoRI; Site_2: NotI;
/note="Vector: pcDNA3.1; Site_1: multiple tissues
library made with RNA pooled from multiple tissues
including liver, lung, hypothalamus, pituitary, and
placenta/endometrium."
                                                                                                                                                                                                         7 ;
                                                                                                                                                                            Length 689;
                                                                                                                                                                                                         Indels
                                                                                                                                                                            Query Match
Best Local Similarity 92.0%; Pred. No. 7.2e-124;
Matches 632; Conservative 0; Mismatches 48;
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/organism="Bos taurus"
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10 (Dases 1 to 689)

2 mith, T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wary, J.E. and Keele, J.W.

A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished (2003)

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

Po Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4396

Fax: 402 762 4390

Email: Smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single pass sequencing. Bases called with phred v0.020425.c and trimmed with the aid of the trim_alt option. Vector identified with cross match v0.990329.

Plate: FQY8056 row: B column: 15
Seq primer: TAGAAGGCACTCGAGG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTCGTGGATTTGGGGAGTGGCTCGACTCTATTAAAGACTTTTCCTTAAATTTGCAG-AG 2306
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                                                                                                                                                                                                                                                                                                          362
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                                                                                            ACATTACTATTGAATCAGCCTTTTTGGAGCTGTTTGTCCTCAGACTTTCCATCAGGTCA
                                                                                                                                                       ACAGACTCAACACCCAGAGATCTTGATTATTCCAGATACTGTCCCCACTGACCAGGCTGCT
                                                                                                                                                                          183 ACAGACTCAACACCCAGAGATCTTGATTATTCCAGATACTGTCCCACTGACCAGGCTGCT
                                                                                                                                                                                                                  2008 GCAGGCACAGATGCTGAGCATGTGCAACAATTCTACAACCTCCTGACAGCCTCCATTGAT
                                                                                                                                                                                                                                       GCAGGCACAGATGCTGAGCATGTGCAACAATTCTACAACCTCCTGACAGCCTCCATTGAT
                                                                                                                                                                                                                                                                            GTATCCAGAAGCTGGGCAGAAAAGATTCCGGGATTTACTGATCTCCCCAAAGAAGATCAG
                                                                                                                                                                                                                                                                                                     GTATCCAGAAGCTGGGCAGAAAAGATTCCGGGATTTACTGATCTCCCCCAAAGAAGATCAG
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                                 CTGAAAGGGAGGAGGTCGTCTGCCTTCCAAACCAAAGAGCCCCATTACAACAGGAACCT
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Smith T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Smith T.P.L., Roberts, A.J., Echternkamp, S.E., Chitko-McKown, C.G., Wray, J.E. and Keel-J.W.
A second set of bovine ESTs from pooled-tissue normalized libraries Unpublished (2003)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Fat: 402 762 4366
Fax: 402 762 4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called with phred v0.020425.c and
trimmed with the aid of the trim_alt option. Vector identified with
cross match v0.9903129.
Plate: FQY8053 row: I column: 18
Seq primer: TAGAAGGCACAGTCGAGG.
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Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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/dore="Organ: Head; Vector: pYx-Asc; Site 1: EcoR I;
/clone="Organ: Head; Vector: pYx-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonafo, Lennon and Soares, Genome Research, 6:791-886,
1996. Denatured RNA was size fractionated on a 1% agarose
gel.First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAACTGAAT. This library was created for the University
lowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."
                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Irisue Procurement: Dr. James Lin University of Iowa

CDNA Library preparation: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

CONE DISTRIBUTION: DISTRIBUTION INFORMATION Can be found at

http://genome.uiowa.edu/distribution/mousefl.html

This clone was contributed by the Brain Molecular Anatomy Project
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                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
1. (bases 1 to 802)
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                                                                                                                     NIN-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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The following repetitive elements were found in this cDNA sequence: 86-116, >GC_rich#Low_complexity
Seq primer: pYX-5,
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85.6%; Pred. No. 1.2e-123;
cive 0; Mismatches 104;
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musculus (house mouse)
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                                                                                                                                                                                                                                                                     524 CACTGCTGAAGATAAGTTTGTGTTCTGCAATGGACTTGTCCTGCATCGACTTCAGTGCCT
                                                                                                                                                                                                                                                                                                                              464 TCGTGGATTTGGGGAGTGGCTCGACTCCATTAAAGACTTTTCTTTAAGTTTGCAGAGCTT
                                                                                                          Gaps
Library made with RNA pooled from multiple tissues including liver, lung, hypothalamus, pituitary, and placenta/endometrium."
                                                                                                         1;
                                                                            Query Match
14.6%; Score 552.6; DB 6; Length 644;
Best Local Similarity 92.2%; Pred. No. 5.3e-123;
Matches 593; Conservative 0; Mismatches 49; Indels 1;
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This invention relates to a novel method for examining allergic diseases that comprises comparing the expression levels of a gene encoding the NOR -1 receptor protein between patients and healthy individuals. Specifically, the NOR-1 gene, also referred to as MINOR, is expressed in the specialist white blood cells known as eosinophils and is involved in mediating an allergic reaction. The present invention describes a differential display method that can identify the expression level of this gene in order to identify its usefulness in diagnosing allergic diseases such as atopic dermatitie. Furthermore, compositions can also be used to screen compounds for the treatment of allergic diseases. Accordingly, they exhibit various activities including antiallergic,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human; receptor; allergic disease; NOR-1; MINOR; eosinophil; atopic dermatitis; antiallergic; antiinflammatory; dermatological.
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                             ADB8398
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(NIGE-) JAPAN GEN AGENCY NATION.
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Costigan M;

Befort K,

D'urso D,

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The invention discloses a composition comprising two or more isolated rat or human polymuclectides or a polymuclectide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polymuclectide, a host cell comprising the vector identifying a nuclectide sequence which is differentially regulated in an animal subjected to pain and a comprising the vector of the polymuclectide sequence that increases or decreases the expression of the polymuclectide sequence that is differentially expressed in neuronal tissue of a first animal companing an earload for identifying a compound which regulates the expression of a polymuclectide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the cativity in an animal of one or more of the polympetides or their antibodies. The polymoclectide or the compound that composition a method for identifying a compound useful in treating conditions are activity is useful for preparing a medicament for treating conditions are civity is useful for preparing a medicament for treating conditions. The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: the specification but was obtained in electronic form directly from WIPO at envisor in the contract of the printed or the compound of the contract of the printed or the compound that contract of the printed or the sequence date for this patent did not form part of the printed or the specification which is differentially expressed during pain.
                                                                                                                                                                                                                                                                                                                              New composition comprising two or more isolated polypeptides, useful preparing a medicament for treating pain in an animal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page; 1017pp; English
                                                                                  01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                  14-AUG-2002; 2002WO-US025765
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antiinflammatory and dermatological. This polypeptide sequence is the human NOR-1 protein sequence of the invention.
                                                                                                                                                           Gaps
                                                                                                                                                           ;
                                                                                                              Length 626;
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                                                                                                            Query Match 100.0%; Score 3337; DB 8; Best Local Similarity 100.0%; Pred. No. 1.6e-222; Matches 626; Conservative 0; Mismatches 0;
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99.9%; Score 3333; DB 7;
99.8%; Pred. No. 3.1e-222;
tive 0; Mismatches 1;
                                          Matches 625; Conservative
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Human, pain, neuronal tissue; gene therapy; spinal segmental nerve injury; chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

WO2003016475-A2.

27-FEB-2003

Homo sapiens

Human Protein Q92570, SEQ ID NO 11667

(first entry)

29-JAN-2004

ADD45995;

ADD45995 standard; protein; 626

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                                                                                                                                                                                                 SMITERHGLKEPKRVEELCNKITSSLKOHOSKGOALEPTESKVLGALVELRKICTLGLOR
          COHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCPVDKRRRNRCQYCRFQKCLSVGMVKE
                      CQHYGVRTCEGCKGFPKRTVQKNAKYVCLANKNCPVDKRRRNRCQYCRFQKCLSVGMVKE
                                                     VVRTDSLKGRRGRLPSKPKSPLQQEPSQPSPPSPPICMMNALVRALTDSTPRDLDYSRYC
                                                                 VVRTDSLKGRRGRLPSKPKSPLQQEPSQPSPPSPPICMMNALVRALTDSTPRDLDYSRYC
                                                                                                                                                            RESIRSNTAEDKFVFCNGLVLHREQCLRGFGEWEDSIKDFSLNLGSLNEDIQALACLSAL
                                                                                                PTDQAAAGTDAEHVQQFYNLLTASIDVSRSWAEKIPGFTDLPKEDQTLLIESAFLELFVL
                                                                                                             PTDQAAAGTDAEHVQQFYNLLTASIDVSRSWAEKIPGFTDLPKEDQTLLIESAFLELFVL
                                                                                                                                           RISIRSNTAEDKFVFCNGLVLHRLQCLRGFGEWLDSIKDFSLNLQSLNLDIQALACLSAL
                                                                                                                                                                                     SMITERHGLKEPKRVEELCNKITSSLKDHQSKGQALEPTESKVLGALVELRKICTLGLQR
                                                                                                                                                                                                                                                                                                                                                                                                      nor-1; nuclear receptor; receptor; leukaemia; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                nor-1 nuclear receptor polypeptide Q92570.
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                                                                                                                                                                                                                                                                                                              protein;
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identifying an upregulator of expression of nor-1 and/or nur77, of identifying a compound for the treatment of leukaemia, and of screening for a compound for treatment of leukaemia, and a mouse model for leukaemia comprising a mouse having defective nor-1 and nur77 nucleic acid sequences.
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                                                                                                                                                                                                                                  Length 626;
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Pred. No. 3.1e-222;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                   625; Conservative
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This invention relates to a novel method of determining whether a patient chas an increased risk for developing a disease or disorder which comprises determining the presence of a mutation or polymorphism in the patient. See John or polymorphism in the patient or level of biological activity of a nuclear receptor expression or level of biological activity of a nuclear receptor polypeptide in the patient or in a cell of the patient. The invention may compared with an antibacterial, antithyroid, cardiovascular-Gen, groopends with an antibacterial, antithyroid, cardiovascular-Gen, groopends with an antibacterial, or insorders-Gen, gastrointestinal-Gen, gracelological, hepatotropic, or pisorders-Gen, gastrointestinal-Gen, gracelological, hepatotropic, or increased risk for developing a disease or disorder. The nucleic acid concerning a disease or disorder. The nucleic acid concerning a disease or disorder, or a compound that increased risk for developing a disease or disorder, or a compound that conding a nuclear receptor polypeptide, an expression vector comprising the nucleic acid operably linked to a promoter, or a compound that candiovascular, intestine, kidney, liver, lung, muscular, gland, colon, cardiovascular, intestine, kidney, liver, lung, muscular, cuterus, panceres, skin, spleen, stomach, testes, thymus, chycoid, or nutritive disease or disorder. The present sequence is that of a nuclear receptor protein which may be used in the method of the
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                                                                                                                                                                                                                                                                                                                                                                                                      Determining an increased risk for e.g. colon, brain or breast disease or disorder, by detecting a mutation or polymorphism in the nuclear receptor gene, or measuring expression or biological activity level of the nuclear
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prostate; skin; spleen; stomach; testes; thymus; thyroid; uterus; panoreas; bone; joint; breast; immune system; metabolic; nutritive disease; human.
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Zeng H;
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Vassilatis D,
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Pred. No. 3.1e-222;
0; Mismatches 1;
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Pavlova MN,
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Best Local Similarity 99.8%;
Matches 625; Conservative C
                                                                                                                                                                                                                            14-NOV-2002; 2002US-0426305P
                                                                                                                                                                                          L2-NOV-2003; 2003WO-US036229
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Madisen L, Mcilwain KL,
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                                                                                                                                                                                                                                                                  (NURA-) NURA INC.
                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ADPO5710
                                                                                                                    WO2004045369-A2
                                                                                   sapiens.
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                                                                                                                                                                                                                                                  PTDQAAAGTDAEHVQQFYNLLTASIDVSRSWAEKIPGFTDLPKEDQTLLIESAFLELFVL
                                                                                                                                                                                                                                                                                                                                                               RLSIRSNTAEDKFVFCNGLVLHRLQCLRGFGEWLDSIKDFSLNLQSLNLDIQALACLSAL
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HPYGLPLAKRAAPLAFPPLGLTPSPTASSLLGESPSLPSPPSRSSSSGEGTCAVGDNAA
                                                   HPYGLPLAKRAAPLAFPPLGLTPSPTASSLLGESPSLPSPPSRSSSSGEGTCAVCGDNAA
                                                                                                          COHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCPVDKRRRNRCQYCRFQKCLSVGMVKE
                                                                                                                                       VVRTDSLKGRRGRLPSKPKSPLQQEPSQPSPPSPPICMMNALVRALTDSTPRDLDYSRYC
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10-SEP-2002; 2002US-0410354P.
12-SEP-2002; 2002US-0410320P.
16-SEP-2002; 2002US-0411766P.
23-SEP-2002; 2002US-0412766P.
23-SEP-2002; 2002US-041285P.
24-SEP-2002; 2002US-041342P.
30-SEP-2002; 2002US-0413432P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADL57171 standard; protein; 626
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The invention relates to a novel isolated polypeptide (NOVX) comprising a mature form of any of the 37 amino acid sequences fully defined in the predictication. A polypeptide of the invention has antidabetic, anorectic, cardiant, hypotensive, antiarterisoclerotic, anorectic, cardiant, hypotensive, antidarterisoclerotic, anorectic, cardiant, hypotensive, antidarterisoclerotic, anorectic, cardiant, hypotensive, anticonvulsant, osteopathic, neuroprotective, antiparkinatory, dermatological, antiasthmatic, and cardiant the manufacture of a medicament for tracting a syndrome associated with a human disease, preferably a NOVX-associated disorder. The mortler acid molecules, polypeptides and antibodies are useful for treating preventing or disgnosing diseases such as metabolic disorders. The nucleic acid molecules, polypeptides and antibodies are useful for treating preventing or disgnosing diseases such as metabolic disorders, clabetes, obesity, infectious diseases (viral, bacterial, fungal, classes, pellepsy, immune disorders, althemer's disease. Parkinson's disease, epilepsy, immune disorders, althemer's classes. Parkinson's disease, epilepsy, immune disorders, althemer's disease. Parkinson's disease, epilepsy, immune disorders, althemer's classes. Parkinson's disease, epilepsy, immune disorders, astham, and various dyslipidesmias. The mucleic acids and polypeptides construction of small molecules cather and various dyslipidesmias. The mucleic acids and polypeptides construction of antibodies that bind immunospecifically to NoVX substances for use in therapeutic or disanseis, cell differation, benatopolesis, wound healing and angiogenesis, in chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The NoVA shows homology to complement factor I precursor; NOV3 shows homology to citanomy precursor; NOV3 shows homology to citanomy processor; NOV3 shows homology to Livy processor; NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               morphin precursor. The present sequence represents a NOVX polypeptide
                                                                                                   isolated NOVX polypeptides and polynucleotides, useful for venting, diagnosing or treating NOVX-associated disorders, e.g. coarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MPCVQAQYSPSPPGSSYAAQTYSSEYTTEIMNPDYTKLTMDLGSTEITATATTSLPSIST
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  Rieger DK;
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  Padigaru M,
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1; Mismatches 3;
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H
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Ort
Anderson DW,
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                                                                                                                                                                    asthma, or infections
                                      WPI; 2004-315567/29.
N-PSDB; ADL57170.
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Matches 622; Conserv
Guo X,
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                                                                                                                           preventing, diaç
osteoarthritis,
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Zhong M,
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PTVAGARFPLFHFKPSPPHPPAPSPAGGHHLGYDPTAAAALSLPLGAAAAAGSQAAALES 240

PTVAGARFPLFHFKPSPPHPPAPSPAGGHHLGYDPTAAAALSLPLGAAAAAGSQAAALEG

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                                                                                                                       361 VVRTDSLKGRRGRLPSKPKSPLQQEPSQPSPPSPPICMMNALVRALTDSTPRDLDYSRYC 420
                                                                                                                                                         PIDQAAAGIDAEHVQQFYNLLIASIDVSRSWAEKIPGFTDLPKEDQTLLIBSAFLELFVL 480
                                                                                                                                                                                    480
                                                                                                                                                                                                                                        540
                                                                                                                                                                                                                                                                   900
                                                                                                                                                                                                                                                                              Human neuron-derived orphan nuclear receptor gene - useful for diagnosing brain diseases such as Alzheimer's or Parkinson's disease or
                                                 COHYGVRICEGCKGFFKRIVOKNAKYVCLANKNCPVDKRRRNRCQYCRFQKCLSVGMVKB 360
                                                                                                      VVRTDSLKGRRGRLPSKPKSPLQQEPSQPSPPSPPICMMNALVRALTDSTPRDLDYSRYC 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, neuron-derived orphan receptor; open reading frame; homology; rat; NOR-1; DNA binding domain; brain; neuronal; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This is the amino acid sequence of a novel human neuron-derived orphan nuclear receptor. The protein has high homology to the rat NOR-1 receptor. The protein contains several DNA binding domains including P, and A boxes which also have high homology to the rat NOR-1 DNA binding
                                                                  CQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCPVDKRRRNRCQYCRFQKCLSVGMVKE
                                                                                                                                                                       SMITERHGLKEPKRVEELCNKITSSLKDHQSKGQALEPTESKVLGALVELRKICTLGLQR
HPYGLPLAKRAAPLAFPPLGLTPSPTASSLLGESPSLPSPPSRSSSSGEGTCAVCGDNAA
                                                                                                                                                                                                               RISIRSNTAEDKFVFCNGLVLHRLQCLRGFGEWLDSIKDFSLNLQSLNLDIQALACLSAL
                                                                                                                                                                                                                                        481 RLSIRSNTAEDKFVFCNGLVLHRLQCLRGFGEWLDSIKDFSLNLQSLNLDIQALACLSAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human neuron-derived orphan receptor NOR-1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "DNA binding domain"
                                                                                                                                                                                                                                                                                                                                  601 IFYLKLEDLVSPPSIIDKLFLDTLPF 626
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                                                                                                                                                                                                                                                                                                                       IFYLKLEDLVSPPSIIDKLFLDTLPF
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                                                                                                                                                                                                                                                                                                                                                                                                                AAW16398 standard; protein; 626
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Parkinson's disease.
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N-PSDB; AAT73334.
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The present invention relates to a new method of treating an organism for an inflammatory immune disease. The method of the invention comprises reducing expression of a NURR subfamily nucleic acid sequence or corticotropin releasing hormone (RH) receptor nucleic acid sequence, inhibiting transcriptional activity of a NURR superfamily member/CRH ceeptor amino acid sequence, or reducing the level of NURR superfamily member/CRH receptor amino acid sequence, or reducing the level of NURR superfamily corganism for an inflammatory immune diseases such as chronic inflammatory joint disease, preferably arthritis, selected from rheumatory corganism for an inflammatory immune diseases such as chronic inflammatory interferes with interaction of a NURR subfamily polypeptide with a cincerferes with interaction of a NURR subfamily polypeptide with a cincerferes with interaction of a NURR subfamily polypeptide and the common response. The agonist of the invention is useful for inhibiting transcriptional activity of nuclear receptor polypeptide and the corresponsit is useful for decreasing the expression of a NURR subfamily antagonist is useful for decreasing the expression of a NURR subfamily creceptor NORI protein of the invention. This sequence is an antagonist of the invention. This sequence is an antagonist of the invention. Dut was obtained from Genbank (7441771)
                                                                                                                                                                                                                                                Treating inflammatory immune disease such as arthritis, comprises suppressing expression level of NURR subfamily of nuclear transcription factors, or corticotropin releasing hormone receptor.
                                                                                                                                          (BAYU ) BAYLOR COLLEGE MEDICINE
                                                                                                                                                                                                                                                                                                                            Claim 2; Page; 123pp; English.
                                                                    11-MAY-2001; 2001WO-US015311
                                                                                                          12-MAY-2000; 2000US-0203645P
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                                                                                                                                                                                                                                                                           FVEGYSSNYELKPSCVYQMQRPLIKVEEGRAPSYHHHHHHHHHHHHHQQQHQQPSIPPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   domains. The nucleic acid and protein can be used to diagnose brain neuronal diseases, e.g. Alzheimer's disease, Parkinson's disease. Further, the genetic diseases can be treated using the receptor as it inhibits expression of a gene by binding to it
                                                                                                                                                                                                     1 MPCVQAQXSBSPPGSSYAAQTYSSEXTTEIMNPDXTKLTMDLGSTEITATATTSLPSIST
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Pred. No. 5e-220;
2; Mismatches 5; Indels
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Best Local Similarity
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Human, nuclear receptor; NURR; inflammatory immune disease; arthritis; corticotropin releasing hormone; receptor; CRH; rheumatoid arthritis; chronic inflammatory joint disease; psoriatic arthritis; thyroiditis; sarcoid arthritis; ulcerative colitis; NOR1.

Homo sapiens

Human nuclear receptor NOR1 protein sequence.

(first entry)

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98.9%;
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             Query Match
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Matches 621; Conservative
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361 VVRTDSLKGRRGRLPSKPKSPLQQEPSQPSPPSPPICMMNALVRALTDSTPRDLDYSRYC
                                                                                     SMITERHGLKEPKRVEELCNKITSSLKDHQSKGQALEPTESKVLGALVELRKICTLGLQR
                                                                                                                                        SMITERHGLKEPKRVEELCNKITSSLKDHOSKGOALEPNESKVLVALVELRKICTLGLOR
                                                                        RLSIRSNTAEDKFVFCNGLVLHRLQCLRGFGEWLDSIKDFSLNLQSLNLDIQALACLSAL
                          PTDQAAAGTDAEHVQQFYNLLTASIDVSRSWAEKIPGFTDLPKEDQTLLIESAFLELFVL
                                        PIDQAAAGTDAEHVQQFYNLLIASIDVSRSWAERIPGFTDLPKEDQTLLIESAFLEL-VL
                                                                                                                                                                                                                                                                                                                                                                Human; nor-1; nuclear receptor; receptor; leukaemia; gene therapy; cytostatic; haematopoietic cell.
                                                                                                                                                                                                                                                                                                                                         Human nor-1 nuclear receptor polypeptide 744171.
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   625;
   Length
                                                            Indels
Score 3299.5; DB 7
Pred. No. 6.4e-220;
1; Mismatches 3;
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WPI; 2003-854017/79.
GENBANK; CAA09763.
                                                                                                 Similarity
                                                                                        Sequence 643 AA;
                                                                                   acid sequences.
                                                                                                 Best Local Sim
Matches 594;
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(GETH) GENENTECH INC WPI; 2004-329389/30. N-PSDB; ADL83261. Similarity Clark H, Sequence 587 AA; WO2004024097-A2 Best Local Simi Matches 586; 17-JUN-2004 25-MAR-2004 40 Query Match 584 601 ADL83262; Chiu H, Wu TD; Homo ADL83262 RESULT g 8 ద ò The present sequence is that of pig nor-1 nuclear receptor polypeptide (2AA09763. Nor-1 has been identified as a molecular target for therapeutic changes. Nor-1 has been identified as a molecular target for therapeutic intervention in the treatment of myeloid leukaemia. The invention composition of a haematopoietic myeloid cell by modulating the level of a nor-1 and/or nur77 nuclear receptor. This involves increasing the level of the receptor polypeptide or polynucleotide, e.g. by administration of a vector comprising the polynucleotide. A claimed method of treating leukaemia comprises modulating a nor-1 and/or nur77 nuclear receptor in a leukaemia comprises modulating cell. Also claimed are methods of identifying a compound for the treatment of leukaemia, and of screening for a compound for the treatment of leukaemia, and of screening for a compound for treatment of leukaemia, and a mouse model for a compound for treatment of leukaemia, and a mouse model for a compound for treatment of leukaemia, and a mouse model for a compound for treatment of nor-1 and nur77 nucleic э ; RALTDSTPRDLDYSRYCPTDQAAAGTDAEHVQQFYNLLTASIDVSRSWAEKIPGFTDLPK 463 RALTDSTPRDLDYSRYCPADQAAAGTDAEHVQQFYNLLTASIDVSRSWAEKIPGFTDLPK 480 EDQTLLIESAFLELFVLRLSIRSNTAEDKFVFCNGLVLHRLQCLRGFGEWLDSIKDFSLN 523 524 LOSLNLDIQALACLSALSMITERHGLKEPKRVBELCNKITSSLKDHQSKGQALEPTESKV 583 FVEGYSSNYELKPSCVYOMO----RPLIKVEEGRAPSYHHHHHHHHHHHHHHHQQ----- 110 120 168 180 226 283 300 343 403 9 9 Inhibiting proliferation of a hematopoietic cell, useful for treating or preventing leukemia, comprises modulating the level or activity of nor-1 and/or nur77 nuclear receptor. EDQTLLIESAFLELFVLRLSIRSNTAEDKFVFCNGLVLHRLQCLRGFGEWLDSIKDFSLR PGPLLDPPMKAVPTVAGARFPLFHFKPSPPHPPAPSPAGGHHLGYDPTAAAALSLPLG--61 FMEGYSSNYELKPSCLYQMQPSGPRPLIKMEEGRAHGYHHHHHDHHHHHHQQQQQQPP -- QHQQPSIPPASSPEDEVLPSTSMYFKQSPPSTPTTPAFPPQAGALWDEALPSAPGCIA 241 AAAAAAAAGSQAAALEGHPYGLPKRAAALAFSPLGLTTSPTTSSLGESPSLPSPPNR SSSSGEGTCAVCGDNAACQHYGVRTCEGCKGFFKRTVQXNAKYVCLANKNCPVDKRRRNR CQYCRFQKCLSVGMVKEVVRTDSLKGRRGRLPSKPKSPLQQRPSQPSPPSPPICMMALV ---AAAAAGSQAAALESHPYGLPLAKRAAPLAFPPLGLTPSPTASSLLGESPSLPSPSR 1 MPCVQAQYSPSPPGSSYAAQTYSSEYTTEIMNPDYTKLTMDLGSTEITATATTSLPSIST Gaps 17; 93.9%; Score 3133.5; DB 7; Length 643; 92.4%; Pred. No. 2.1e-208; ive 10; Mismatches 22; Indels 17; Disclosure; SEQ ID NO 17; 101pp; English. Milbrandt J; (BAYU) BAYLOR COLLEGE MEDICINE (UNIW) UNIV WASHINGTON. Mullican SE, Conneely OM, Conservative 404 421 464

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The present invention relates to PRO proteins and their coding sequences.

The PRO proteins are useful for diagnosing and treating a B cell related disorder, e.g. X-linked infantile hypogammaglobulinemia, polyaeccharide antigen unresponsiveness, selective IgA deficiency, selective IgA deficiency, selective IgA deficiency, beneficiency, burkit's configuration, transient hypogammaglobulinemia of infancy, Burkit's urknemediate lymphoma, follicular lymphoma, tutermediate lymphoma, follicular lymphoma, type II charmediate lymphoma, follicular lymphoma, type II charmediate lymphoma, tollicular lymphoma, type II charmediate lymphoma, tollicular lymphoma, type II charmediate lymphoma, projement of arthitis, autoimmune mediated haemolytic anaemia, myasthenia gravis, hypoadrenocorticism, glomerulonephritis, or ankylosing spondylitis. The PRO protein are also useful for preparing a condition that is responsive to the PRO protein, e.g. cancer or immune-mediated inflammatory diseases. The PRO coding sequences are useful as hybridization probes in chromosome and come mapping, in preparing PRO proteins, or in generating transgenic animals or knockout animals, which in turn are useful in the development can are screening of therapeutically useful reagents.
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Immunosuppressive; Cytostatic; Antiarthritic; Antirheumatic; Antianemic; Antiallergic; Muscular; Neuroprotective; Nephrotropic; Antiinflammatory; Gene Therapy; PRO; B cell related disorder; cancer; immune-mediated inflammatory disease; human.
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                                                                                                                        626
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                                                                                                                                                              LRALVELRKICTLGLQRIFYLKUEDLVSPPSIIDKLFLDTLPF
                                                                                                                            LGALVELRKICTLGLQRIFYLKLEDLVSPPSIIDKLFLDTLPF
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                                                                                                                                                                                                                                                                                                                                                                                     ADL83262 standard; protein; 587
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illarity 99.8%;
Conservative 0
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                                                                                                                                                                                                                                                                             FSLNLQSLNLDIQALACLSALSMITERHGLKEPKRVEELCNKIISSLKDHQSKGQALEPT
             HHTHHTHHQQQQQQQDSIPPASSPEDEVLPSTSMYFKQSPPSTPTPAFPPQAGALWDEA
                                                                ALSIPIGAAAAAGSQAAALESHPYGIPIAKRAAPIAFPPIGITPSPTASSILGESPSIPS
                                                                                                                                                                                 241 PPSRSSSSSGGTCAVCGDNAACQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCPVDKR
                                                 LPSAPGCIAPGPLLDPPMKAVPTVAGARFPLFHFKPSPPHPPAPSPAGGHHLGYDPTAAA
                                                                                                                      RRNRCQYCRFQKCLSVGMVKEVVRTDSLKGRRGRLPSKPKSPLQQEPSQPSPPSPPICMM
                                                                                                                                                                                                                                                                                                                  DLPKEDQTLLIESAFLELFVLRLSIRSNTAEDKFVFCNGLVLHRLQCLRGFGEWLDSIKD
                                                                                                                                                                                                                                                                                                                                                                      FSLNLQSLNLDIQALACLSALSMITERHGLKEPKRVEELCNKITSSLKDHQSKGQALEPT
HHHHHHHHHQQQHQQPSIPPASSPEDEVLPSTSMYFKQSPPSTPTTPAFPPQAGALWDEA
                                                                                                                                                                                                                                                               NALVRALTDSTPRDLDYSRYCPTDQAAGGTDAEHVQQFYNLLTASIDVSRSWAEKIPGFT
                                                                                                                                                                                                                                                                                                                                                                                                                         ESKVLGALVELRKICTLGLQRIFYLKLEDLVSPPSIIDKLFLDTLPF 626
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WP-kappaB pathway; antiinflammatory; cytostatic; hepatotropic; virucide; antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic; antiarthritic; antirheumatic; gastrointestinal-Gen; antiasthmatic; antiarterioscalerotic; immunomodulator; cerebroprotective; vasotropic; imflammatory disorder; NP-kappaB regulation; cancer; aberrant apoptosis; inflammatory disorder; NP-kappaB regulation; cancer; aberrant apoptosis; where to disorder; Hodgkin's lymphoma; haematopoietic tumour; hyporidrotic ectodermal dysplasia; whyper-IgM syndrome; hypoinfarotic ectodermal dysplasia; wiral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza; viral infection; HIV-1; HTLV-1; hepatitis B; hepatitis C; EBV; influenza; wiral infection; anthiamatory bowel disease; colitis; asthma; thermatorid arthritis; inflammatory bowel disease; colitis; asthma; atherosclerosis; cachexia; euthyroid sick syndrome; stroke; EAE; autoimmune disorder; hyper immune activity; autoimmune disorder; hyper congenital condition; birth defect; mecrotic lesion; wound; organ transplant rejection; wound; organ transplant rejection; whereant eighal transduction; proliferating disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HIV propagation; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO2004065577-A2
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240 339 RRNRCQYCRFQKCLSVGMVKEVVRTDSLKGRRGRLPSKPKSPLQQEPSQPSPPSPPICWM 3999

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13-JAN-2004; 2004WO-US000798

241 PPSRSSSSGEGTCAVCGDNAACQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCPVDKR 300

PPSRSSSGEGTCAVCGDNAACQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCPVDKR

ALSLPLGAAAAAGSQAAALEGHPYGLPLAKRAAPLAFPPLGLTPSPTASSLLGESPSLPS

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This invention relates to the novel association of protein sequences (and the genes which encode them) to the NP-kappaB pathway. The invention may the genes which encode them) to the NP-kappaB pathway. The invention may cytostatic, hepatotropic, virucide, antiarteriosclerotic, antiarteriosclerotic, cytostatic, hepatotropic, virucide, antiarteriosclerotic, antiarteriosclerotic, immunomodulator, cerebroprotective, vasotropic, immunosuppressive or cyulnerary activity or for gene therapy. The proteins and nucleotides are useful for diagnosing, preventing, treating, or ameliorating conditions conditions are useful for diagnosing, preventing, treating, or ameliorating conditions in immune disorder, an inflammatory disorder, an inflammatory disorder.

Condition aberrant NP-kappaB required, cancer, aberrant apportosis, related to aberrant NP-kappaB required, cancer, aberrant apportosis, condermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1, expodermal dysplasia, immunodeficiency, viral infections, HIV-1, HTLV-1, condermal dysplasia, immunodeficiency, viral infection, host cells our vival, evasion of immune responses, rheumatoid arthritis, inflammatory condermined is activity, disorders related to aberrant actue phase responses, hypercongenital conditions, birth defects, necrotic lesions, wounds, organ transplant rejection, conditions related to oberrant signal transplant conditions, birth defects, necrotic lesions, wounds, organ transplant rejection, conditions related to operant acute phase responses, hypercongenital conditions, birth defects, necrotic lesions, wounds, organ transplant rejection, conditions related to operant acute phase, collise acuted to aberrant signal transduction, which other viruses. The present sequence is that of a human protein which the viruses. The present sequence is that of a human protein which invention. Note: This sequence does not appear in the specification with the NP-kappaB pathway of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 159
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                                                                                                                                                                                                                                                            New isolated polynuclectides and polypeptides associated with NF-kappaB pathway, useful for diagnosing, treating, or preventing disorders or diseases associated with NF-kappaB pathway.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MDLGSTEITATATTSLPSISTFVEGYSSNYELKPSCVYQWQRPLIKVEEGRAPSYHHHHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 220 ALSLPLGAAAAAGSQAAALESHPYGLPLAKRAAPLAFPPLGLTPSPTASSLLGESPSLPS
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                                                                                                                                             Carman J;
                                                                                                                                                                                                                                                                                                                                                               Claim 6; SEQ ID NO 64; 237pp; English.
                                                                                                                                             Feder JN,
                                                                                             (BRIM ) BRISTOL-MYERS SQUIBB CO
                    14-JAN-2003; 2003US-0440068P.
12-MAY-2003; 2003US-0469757P.
                                                                                                                                             Neubauer MG,
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                                                                                                                                                                                             WPI; 2004-562168/54
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                                                                                                                                             Nadler SG,
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IPPASSPEDEVLPSTSMYFKQSPPSTPTTPAFPPQAGALWDEALPSAPGCIAPGPLLDPP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine; NOR1; neuroleptic; Neural Orphan Receptor 1;
Translocated in Extraskeletal Chondrosarcoma; TEC; cell proliferation;
apoptosis; central nervous system; transgenic mouse;
pain response threshold; impaired balance; impaired motor coordination.
                                                                                                                                                                                                                                                                                                                                                                     CLSALSMITERHGLKEPKRVEELCNKITSSLKDHQSKGQALEPTESKVLGALVELRKICT
                                                                                                                                                                                                                                                                  416 YSRYCPTDOAAAGTDAEHVOOFYNLLTASIDVSRSWAEKIPGFTDLPKEDOTLLIESAFL
                                                                                                                                                                                                                                                                                                             ELFVLRI,SIRSNTAEDKFVFCNGLVLHRIQCLRGFGEWLDSIKDFSLNLQSLALDIQALA
                GDNAACQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCPVDKRRNRCQYCRFQKCLSV
                                                                                                                                                                                          GDNAACQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCPVDKRRRNRCQYCRFQKCLSV
                                                                                                                                                                                                                       GMVKEVVRTDSLKGRRGRLPSKPKSPLQQEPSQPSPPSPPICMMNALVRALTDSTPRDLD
                                                                                                                                                                                                                                     177 MKAVPTV-AGARFPLFHFKFSPPHPPAPSPAGGHHLGYDPTAAAALSLPLGAAAAAGSQA
                                                                                                      AALESHPYGLPLAKRAAPLAFPPLGLTPSPTASSLLGESPSLPSPPSRSSSGEGTCAVC
    PVEGYSSNYELKPSCVYQM----ORPLIKVEEGRAPSYHHHHHHHHHHHHHOQOHQOPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine Neural Orphan Receptor 1, NOR1, #2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB98438 standard; protein; 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-DEC-2000; 2000US-0251794P.
24-SEP-2001; 2001US-0324614P.
04-DEC-2001; 2001US-00005169.
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ABB98438
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                                                                                                                                                                                                                                                                                                                    Rat nuclear receptor gene; embryo; cerebral neuron; induction; apoptosis; amplification; primer; PCR; Antisense; ribozyme; nerve; disease.
                                       DLPKEDQTLLIESAFLELFVLRLSIRSNTAEDKFVFCNGLVLHRLQCLRGFGEWLDSIKD 519
                                                                            579
                      459
RRNRCQYCRFQKCLSVGMVKEVVRTDSLKGRRGRLPSKPKSPLQQEPSQPSPPSPPICMM 36,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MPCVQAQYSPSPPGSSYAAQTYSSEYTTEIMNPDYTKLTMDLGSTEITATATTSLPSIST
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                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
293. .628
/note= "DNA binding domain"
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N-PSDB; AAT16151.
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475 477

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235 237 295 297 355 357

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595 597

(first entry)

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New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                                                               in; neuronal tissue; gene therapy; spinal segmental nerve injury; constriction injury; CCI; spared nerve injury; SNI; Chung.
                                                       Rat Protein P51179, SEQ ID NO 11665
                                                                                                                                                                                                                                  14-AUG-2001; 2001US-0312147P.
01-NOV-2001; 2001US-0346382P.
26-NOV-2001; 2001US-0333347P.
                                                                                                                                                                                                        14-AUG-2002; 2002WO-US025765
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                                                                                                                        Rattus norvegicus
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                                       Novel targeting construct for producing transgenic mouse useful as disease model and for identifying modulators of gene expression, has sequences homologous to neural orphan receptor 1 and a selectable marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                          IPPASSPEDEVLPSTSMYFKQSPPSTPTTPAFPPQAGALWDBALPSAPGCIAPGPLLDPP 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AALESHPYGLPLAKRAAPLAFPPLGLTPSPTASSLLGESPSLPSPPSRSSSSGEGTCAVC 295
                                                                                                                    The present sequence is a protein sequence for murine Neural Orphan Receptor 1 (NOR1, also known as Translocated in Extraskeletal Chondrosarcoma (TEC), is involved in the control of cell proliferation and apoptosis and is expressed mainly in the central nervous system. The NOR1 coding sequence was used to generate a targeting construct (I). (I) is useful for producing a transgenic mouse comprising a disruption in a NOR1 gene and exhibiting increased or enhanced pain response threshold, or impaired balance and impaired motor coordination
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                                      Novel targeting construct for disease model and for identify
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2002-608255/65
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Best Local Similarity
                                                                                                                                                                                                                                                Sequence 628 AA;
                                                    disease model
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Costigan M;

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cutariary of a maintain of the movel polymucleotide, a host cell comprising the vector comprising the movel polymucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence (C which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polymucleotide sequence (C that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polymucleotide sequence which is differentially a compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the compound that regulates the activity of one or more of the regulates the compound or small molecule that regulates the cativity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating compound that expensions or their antibodies. The polypeptides given in the specification, and a pharmaceutical composition comprising the one or more coplypeptides or their antibodies. The polypeptide or the compound that modulates its activity is useful for preparing a medicament for treating coplypeptides or their antibodies. The polymucleotide or the compound that modulates its activity is useful for preparing a medicament for treating copin, (CI) and spared nerve injury (SNI) in an animal (e.g. sphan contribution) which is differentially expressed during patent of new propersor of the printed copin who was obtained in electronic form directly from WIPO at the wipo.int/pub/published_pot_sequence.
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                                                                                The invention discloses a composition comprising two or more isolated or human polynucleotides or a polynucleotide which represents a fragme derivative or allelic variation of the nucleic acid sequence. Also
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Claim 1; Page; 1017pp; English
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ADD45993 standard; protein; 628

RESULT 14 ADD45993 ID ADD4 XX

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                                                                                                                                                                               417
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                                   MKAVPTV-AGARFPLFHFKPSPPHPPAPSPAGGHHLGYDPTAAAALSLPLGAAAAAGSQA 235
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                         IPPASSPEDBVLPSTSMYFKQSPPSTPTTPAFPPQAGALWDEALPSAPGCIAPGPLLDPP 176
                                                                                                                             YSRYCPTDQAAAGTDAEHVQQFYNLLTASIDVSRSWAEKIPGFTDLPKEDQTLLIESAFL
                                                                                                                                                                                                         CLSALSMITERHGLKEPKRVEELCNKITSSLKDHQSKGQALEPTESKVLGALVELRKICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                 gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                 nuclear receptor; receptor; leukaemia; haematopoietic cell.
                                                                                                                                                                                                                                                                                                                                                                                                                 nor-1 nuclear receptor polypeptide JC2493
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                                                                                                                                                                                                                                                                                                              QGLQRIFYLKLEDLVSPPSVIDKLFLDTLPF
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The present sequence is that of rat nor-1 nuclear receptor polypeptide CC JC2493. Nor-1 has been identified as a molecular target for therapeutic intervention in the treatment of myeloid leukaemia. The invention provides methods of inhibiting the proliferation of a haematopoietic stem cell or a haematopoietic myeloid cell by modulating the level of a nor-1 and/or nur7 nuclear receptor. This involves increasing the level of the receptor polypeptide or polynucleotide. A claimed method of treating corporations modulating a nor-1 and/or nur77 nuclear receptor in a leukaemia comprises modulating a nor-1 and/or nur77 nuclear receptor in a cleaning to myeloid cell. Also claimed are methods of claimed are methods of identifying a compound for the treatment of leukaemia, and of screening identifying a compound for the treatment of leukaemia, and of screening cleukaemia comprising a mouse having defective nor-1 and nur77 nucleic
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llarity 92.2%; Pred. No. 2.7e-204;
Conservative 12; Mismatches 29;
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ORGANISM: Human
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10, Appl
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                                                               March 12, 2005, 17:42:07; Search time 42 Seconds (without alignments) 1112.627 Million cell updates/sec
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Sequence 3
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3337
1 MPCVQAQYSPSPPGSSYAAQ......EDLVSPPSIIDKLFLDTLPF
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-949-016-6699
US-09-949-016-10338
US-09-277-078-2
US-07-952-800-2
US-07-952-800-2
US-08-592-183-2
US-08-095-728B-4
PCT-US92-02320A-4
US-08-764-870-7
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US-08-980-115-7
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US-08-16-92A-2
US-08-593-383-4
US-09-949-016-11665
US-08-336-40BB-2
US-08-36-40BB-2
US-08-76-870-6
US-08-76-980-115-6
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PCT-US91-00399-2
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Maximum Match 100%
Listing first 45 summaries
                                            - protein search, using sw model
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US-09-949-016-9660
; Sequence 9660, Application US/09949016
; Sequence 9660, Application US/09949016
; Patent No. 6812339
; BAREAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; FILE REFERENCE: CLOO1307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT PILING DATE: 2000-10-14
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SEQ ID NOS: 207012
; SEQ ID NO 9660
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Sequence 8941, Ap Sequence 6009, Ap Sequence 6009, Ap Patent No. 5223606 Sequence 8939, Ap Sequence 8940, Ap Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 5, Appli Sequence 10, 2560432
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Sequence 8,
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100.0%; Pred. No. 6.7e-249;
ive 0; Mismatches 0;
US-09-949-016-8941
US-09-949-016-8942
US-09-949-016-6009
5223606-2
5225606-2
US-09-949-016-8939
US-09-949-016-8939
US-09-949-016-8940
US-08-336-408B-6
PCT-US91-00399-6
PCT-US91-00399-6
US-08-216-592A-6
PCT-US91-00399-4
US-08-764-9115-5
526432-2
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US-08-91-220-4
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US-08-216-592A-8
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Sequence 6699, Application.US/09949016
; Sequence 6691339
; GENERAL INFORMATION:
; APPLICANT VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLOO1307
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR PELING DATE: 2000-10-20
; PRIOR PELING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-04
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
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                       PIDQAAACTDAEHVOOPYNLLIASIDVSRSWAEKIPGFTDLPKEDQTLLIESAPLELFVL
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                                                                                 VVRTDSLKGRRGRLPSKPKSPLQQEPSQPSPPSPPICMMNALVRALTDSTPRDLDYSRYC
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54.5%; Pred. No. 1.1e-126;
cive 74; Mismatches 121;
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US-09-949-016-6699
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FACENTE OF TOTAL TREATH NO. 1815.31;
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    HPYGLPLAKRAAPLAFPPLGLTPSPTASSLLGESPSLPSPPSRSSSSGEGTCAVCGDNAA
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99.4%; Score 3316; DB 4; Length 626;
Best Local Similarity 99.4%; Pred. No. 2.4e-247;
Matches 622; Conservative 1; Mismatches 3; Indels
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Patent No. 6812339
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Sequence 10263, Application US/09949016

Patent No. 6812339

GENERAL INPORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOCTAME: FastSEQ for Windows Version 4.0

SEQ ID NO 10263
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                                GHHLGYDPTAAAALSLPLGAAAAGSQAAALESHPYGLP-LAKRAAPLAFPPLGLTPSPT 266
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96 PSTFWDGYTGEFD---TFLYQLPGTVQPCSSASSSASSASSSATSPASASFKFEDFQVY 152
168 LHNFHQNYVATTHMIEQRKTPVSRLSLFSFKQSPPGTPVSSCQMRFDGPLHVPMNPEPAG 227
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                                                      ASSLIGESPSIPSPSRSSSGEGTCAVCGDNAACQHYGVRTCEGCKGFFKRTVQKNAKY
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41.0%; Score 1367; DB 4; Length 641;
Best Local Similarity 47.5%; Pred. No. 4.7e-97;
Matches 317; Conservative 74; Mismatches 165; Indels 112;
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US-09-949-016-10263
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Fatent No. 6812339

GENERAL INFORMATION:
FALLE OF INVENTION:
TITLE OF INVENTION:
FILLE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 00/241,755

FRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

FRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOUTH OF SEQ ID NOS: 207012

SEQ ID NO 10338
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                                                                              387 SQPSPPSPPICMMNALVRALTDSTP--RDLDYSRY-CPTDQAAAGTDAEHVQQFYNLLTA
                                                                                                                                                                                                                         LOCLRGFGEWLDSIKDFSLNLQSLNLDIQALACLSALSMITERHGLKEPKRVEELCNKIT
                                                                                                                                                                                                                                                                                                                  533 NCLKDHVTFNNGGLNRPNYLSKLIGKLPELRTLCTQGLQRIFYLKLEDLVPPPAIIDKLF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MPCVQAQYSPSPPGSSYAAQTY----SSEYTTEIMNPDYTKLTWDLGSTEITATATTSLP
                                SSLKDHQ--SKGQALEPTE-SKVLGALVELRKICTLGLQRIFYLKLEDLVSPPSIIDKLF
                ASSLIGESPSLPSPPSRSSSSGEGTCAVCGDNAACQHYGVRTCEGCKGFFKRTVQKNAKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                       LDTLPF 626
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US-09-949-016-10338
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Qy	RESULT 7 US-07-952-800-2 US-07-95-800-2	USA DABLE FORM: E: Floppy disk IBM PC compatible SYSTEM: PC-DOS/MS-DOS PATENTIN Release #1.0 ICATION DATA: N UMMBER: US/07/952,8 NT INFORMATION: E: 19920928 NT INFORMATION: GY, Kenneth A ON NUMBER: 31,677 DOCKET NUMBER: 15280- ATION INFORMATION: 415-543-9600 415-543-9600 415-543-5043 R SEQ ID NO: 2: RACTERISTICS: 33 amino acids NO ACID Ilnear	Ouery Match Best Local Similarity 29.7%; Pred. No. 6.8e-33; Best Local Similarity 29.7%; Pred. No. 6.8e-33; Matches 151; Conservative 70; Mismatches 189; Indel8 99; Gaps 17; QY 118 PPASSPEDEVLPSTSMYFKQSPRSTPTTPAPPPQAGALWDEALPSAPGCIAPGPLLDPPM 177 Db 83 PDSSSPNP-LPGGVPPPSPPGPPLEPPSTAPSLGGSGAPPPPPM 124 QY 178 KAVPTVAGARPLFHFKPSPPHPPAPSPAGGHHLGYDPTAAALSLLGAAAAAGSQAAA 237 QY 178 KAVPTVAGARPLFHFKPSPPHPAPSPAGGHHLGYDPTAAAALSLLGAAAAAGSQAAA 237 Db 125 PPPPLGSPFPVISSSMGSPGLPPPAPPGFSGPVSSPQINSTVSLPGGGSG 174
Db 153 GCYPGPLSGPVDEALSSGSDYYGSPCSAPSPSTPSFQPPQLSPWDGSFGHFSPSQTYBG 212 Qy 154 -ALWDEALPSAPGCIAPGPLLDPPMKAVPTVAGARFPLFHFKPSPHPPAPSPAGGHLG 212 Db 213 LRAWTEQLPKASCPPA-FSFSPPTGSPSF244 Qy 213 YDPTAAAALSL-PLGAAAAAGSQAAALESHPYGLPLAKRAAPLAFPPLGLTPSPTASSLL 271 Db 245LAGSPLKLFPSQATHQLGEGESYSMPTAFPGLAPTSPHLE 284 Qy 272 GESPSLPSPSRSSSGEGTCAVCGDNAACQHYGVRTCEGCKGFFKRTVQKNAK 325	Db 400	SULT 6 SQUENCE 2, Sequence 2, Patent No. 6 GENERAL INF APPLICANT:	2 2 2 4

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APPLICANT: Tsai, S. and S.J. Collins
IITLE OF INVENTION: "Hematopoietic Cell Lines Bearing Altered Retinoic Acid Recep
                                                     170 -KKKEVPKPECSESYTLTPEVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDID 228
                                                                                                             HVQQFYNLLTASIDVSRSWAEKIPGFTDLPKEDQTLLIESAFLELFVLRLSIRSNTAEDK 492
                                                                                                                                                                                                     FVFCNGLVLHRLQCLR-GFGEWLDSIKDFSLNLQSLNLDIQALACLSALSMIT-ERHGLK 550
                                                                                                                                                                                                                                                                                                                     349 QPDRVDMLQEPLLEALKVYVRKRRPSRPHMFPKMLMKITDLRSISAKGAERVITLKMBIP 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 PSPAGGHHLGYDPTAAAALSLP--LGAAAAGSQAAALESHPYGLPLAKRAAPLAFPPLG 260
                                                                                                                                                                                                                               BPKRVEELCNKITSSLKDHOSKGOALEP-TESKVLGALVELRKICTLGLORIFYLKLEDL
                       SKPKSPLQQEPSQPSPPSPPICMMNALVR-ALTDSTPRDLDYSRYCP--TDQAAAGTDAE
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15.9%; Score 530.5; DB 2; Length 462;
Best Local Similarity 34.5%; Pred. No. 9.6e-33;
Matches 152; Conservative 64; Mismatches 181; Indels 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Centre, 1420 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 1-206-682-8100; 1-206-224-0709(direct) INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Diskette-5.25 inch, 1.2Mb storage COMPUTER: IBM PC/386 Compatible OPERATING SYSTEM: MS-DOS 4.01 SOFTWARE: Word for Windows 5.01-t CURREMY APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LECULE TYPE: polypeptide
DESCRIPTION: sequence encoded by SEQ. ID. NO.
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                                                                                                                                                                                                                                                                                                                                                                                 610 VSPPSIIDKLF----LDTL 624
                                                                                                                                                                                                                                                                                                                                                                                                                         409 GSMPPLIQEMLENSEGLDTL 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-592-383-2; Sequence 2, Application US/08592383; Patent No. 5830760; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/099,24
FILING DATE: July 28, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Broderick, Thomas F.
REGISTRATION NUMBER: 31,332
REFERENCE/DOCKET NUMBER: FHCR
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MEDIUM TYPE: Diskette
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ITILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: US/09/949,016

FILE REFERENCE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,768

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-10-03
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                                                                                                                                                                                                                                                                                                                                                                                   | :|| :|: : : || : | || : : || 364 PLDDQVILLRAGWNELLIASFSHRSIDVRDGILLATGLHVHRNSAHSAGVGAIFDRVLTE 423
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                                            -------PPEDVKP----PVLGVRGLHCPPPPPGGPGAGKRLCAICGD 210
                                                                                        298 NAACQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCPVDKRRRNRCQYCRFQKCLSVGM 357
                                                                                                                                                                              VKEVVRTDSLKGRRGRLPSKPKSPLQQEPSQPSPPSPPICMMNALVRAL------- 406
                                                                                                                                                                                                       323 GGTGGSGSSPND-----PVTNICQAAD----KQLFTLV-----EWAKRIPHFSSL 363
                                                                                                                                                                                                                                                                                                                                                          PKEDQTLLIESAFLELFVLRLSIRSNTAEDKFVFCNGLVLHRLQC-LRGFGEWLDSI-KD 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                FSLNLQSLNLDIQALACLSALSMIT-ERHGLKEPKRVEELCNKITSSLKDH-QSKGQALE 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203 PSPAGGHHLGYDPTAAAALSLP--LGAAAAAGSQAAALESHPYGLPLAKRAAPLAFPPLG 260
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LESHPYGLPLAKRAAPLAFPPLGLTPSPTASSLLGESPSLPSPPSRSSSGEGTCAVCGD
                                                                                                                                                                                                                                                                    407 ----TDSTPRDLDYSRYCPTDQAAAGTDAEHVQQFYNLLTASIDVSRSWAEKIPGFTDL
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 8178
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CTHER INFORMATION: Xaa = Any Amino Acid
US-09-949-016-8178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8178, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
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US-09-949-016-8178
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REFERENCE/DOCKET NUMBER: 38694-PCT TELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             610 VSPPSIIDKLF----LDTL
                                   Query Match
Best Local Similarity 34.5
Matches 152; Conservative
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STATE: NEW YORK
COUNTRY: U.S.A.
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US-08-095-728B-4
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                                                                           FKRTVQKNAKYVCLANKNCPVDKRRRNRCQYCRFQKCLSVGMVKEVVRTDSLKGRRGRLP 375
                                                                                                                                                                              165 -KKKEVPKPECSESYTLTPEVGELIEKVRKAHQETFPALCQLGKYTTNNSSEQRVSLDID 223
                                                                                                                                                                                                                      433 HVQQFYNLLTASIDVSRSWAEKIPGFTDLPKEDQTLLIESAFLELFVLRLSIRSNTAEDK 492
                                                                                                                                                                                                                                          224 IMDKFSELSTKCIIKTVEFAKQLPGFTTLTIADQITLLKAACLDILILRICTRYTPEQDT 283
                                                                                                                                                                                                                                                                                         493 FVFCNGLVLHRLQCLR-GFGEWLDSIXDFSLNLQSLNLDIQALACLSALSMIT-ERHGLK 550
                                                                                                                                                                                                                                                                                                                  284 MIFSDGLILNRIQMHNAGFGPLTDLVFAFANQLLPLEMDDAETGLLSAICLICGDRQDLE 343
                                                                                                                                                                                                                                                                                                                                                                                       LIPSP----TASSLLGE-SPSLPSPPSRSSSGEGTCAVCGDNAACQHYGVRICEGCKGF 315
                            376 SKPKSPLQQEPSQPSPPSPPICMMNALVR-ALTDSTPRDLDYSRYCP--TDQAAAGTDAE 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4, Application US/08095728B
Sequence 10. 5843642
GENERAL INFORMATION:
APPLICANT: DMITROVSKY, ETHAN
APPLICANT: WARRELL JR, RAYMOND P
APPLICANT: WILLER JR, WILSON H
APPLICANT: FRANKELL, STANLEN
TITLE OF INVENTION: METHODS FOR THE DETECTION AND
TITLE OF INVENTION: TREATMENT OF ACUTE PROMYELOCYTIC LEUKEMIA (APL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (212) 29,678
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 391-0525
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 467
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STREET: 1185 AVENUE OF THE AMERICAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/095,728B
FILING DATE: 21-UUL-1993
CLASSIFICATION: 435
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APPLICATION NUMBER: US 07/673,838
FILING DATE: 22-MAR-1991
ATTONNEY/AGENT INFORMATION:
NAME: WHITE, JOHN P
REGISTRATION NUMBER: 28,678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIF: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | | :| :: | | | | 404 GSMPPLIQEMLENSEGLDTL 423
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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US-08-095-728B-4
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                                                                                                                                                                                                                                                                                                                                                        376 SKPKSPLQQEPSQPSPPSPPICMMNALVR-ALTDSTPRDLDYSRYCP--TDQAAAGTDAE 432
                                                                                                                                                                                                                                                                                                                                                                                       433 HVQQFYNLLTASIDVSRSWAEKIPGFTDLPKEDQTLLIESAFLELFVLRLSIRSNTAEDK 492
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                                                                                  203 PSPAGGHHLGYDPTAAALSLP--LGAAAAGSQAAALESHPYGLPLAKRAAPLAFPPLG 260
                                                                                                                                                                                                                         111
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                                                                                                                                                                                                                                                                                             261 LTPSP----TASSLLGE-SPSLPSPSRSSSGEGTCAVCGDNAACQHYGVRTCEGCKGF
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                                          Gaps
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Sequence 4, Application PC/TUS9202320A
GENERAL INFORMATION:
APPLICANT: Sloan-Kettering Institute, For Cancer Research
TITLE OF INVENTION: METHODS FOR DETECTION AND TREATMENT OF CANCER
INDER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: COOPER & DUNHAM
STREET: 30 ROCKEFELLER PLAZA
                                            43;
Length 462;
                                            Indels
                                            64; Mismatches 181;
  DB 2;
15.9%; Score 530.5; DB 2 34.5%; Pred. No. 9.6e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02320A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 675,084
FILING DATE: 22-MAR-1991
PRIOR APPLICATION NUMBER: US 673,838
FILING DATE: 22-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WHITE, JOHN P
REGISTRATION NUMBER: 28,678
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OPERATING SYSTEM:
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US-08-980-115-7
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                                                                                                                                                                                                       43;
                                                                                                                                                                         Length 462;
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APPLICANT: Scanlar, Thomas S
APPLICANT: Baxter, John D
APPLICANT: Baxter, John D
APPLICANT: Bayer, Schort J
APPLICANT: Wagner, Richard L
APPLICANT: Kushner, Peter J
APPLICANT: Kushner, Peter J
APPLICANT: Wast, Brian
TITLE OF INVENTION: Nuclear Receptor Ligands and Ligand
TITLE OF INVENTION: Binding Domains
MUMBER OP SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward
                                                                                                                                                                                                     Indels
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STREET: Five Palo Alto Square, 3000 El Camino Real
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                    64; Mismatches 181;
                                                                                                                                                                         DB 5;
                                                                                                                                                                                       Pred. No. 9.6e-33,
                                                                                                                                                                        15.9%; Score 530.5; 34.5%; Pred. No. 9.6
, LELEFAX: (212) 644-0525
; TELEX: (212) 644-0525
; INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 aming
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Patent No. 6236946
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                    Matches 152; Conservative
                                                                                                           ; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-02320A-4
                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
US-08-764-870-7
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118 PPASSPEDEVLPSTSMYFKQSPPSTPTTPAFPPQAGALWDEALPSAPGCIAPGPLLDPPM 177
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               PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Nakamura, Jackie N
REGISTRATION NUMBER: 35,966
REFERENCE/DOCKET NUMBER: UCAL-246/01US
TELECOMMUNICATION INFORMATION:
TELECOMMUNE: (650) 843-5000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
SOFTWARE: Patentin Release #1.0, Ver CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/764,870
FILING DATE: 13-DEC-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: US 60/008,540
FILING DATE: 13-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,543
FILING DATE: 13-DEC-1995
PRIOR APPLICATION NUMBER: US 60/008,543
FILING DATE: 14-DEC-1995
APPLICATION NUMBER: US 60/008,606
FILING DATE: 14-DEC-1995
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amino acid
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MOLECULE TYPE: protein
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471 YPEQQGRFAKLLLRLPALRSIGLKCLEHLFFFKL 504
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amino acid
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Best Local Similarity 29.5%
Matches 150; Conservative
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MOLECULE TYPE: protein
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US-08-216-592A-4
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                                                        GENERAL INFORMATION:
APPLICANT: Scanlan, Thomas S.
APPLICANT: Baxter, John D.
APPLICANT: Baxter, John D.
APPLICANT: Baxter, John D.
APPLICANT: Wichaer, Richard L.
APPLICANT: Wagner, Richard L.
APPLICANT: Wagner, Richard L.
APPLICANT: Wagner, Peter J.
APPLICANT: Apriletti, James W.
APPLICANT: Apriletti, James W.
APPLICANT: Shiau, Andrew K.
TITLE OF INVENTION: NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOWAINS
FILE REFERRINCE: UCAL-246/02US
CURRENT FILING DATE: 1997-11-26
EARLIER FILING DATE: 1997-11-13
EARLIER FILING DATE: 1995-12-14
EARLIER FILING DATE: 1995-12-14
EARLIER FILING DATE: 1995-12-13
EARLIER FILING SATE: 1995-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 KAVPTVAGARFPLFHFKPSPPHPPAPSPAGGHHLGYDPTAAAALSLPLGAAAAAGSQAAA 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358 VKEVVRTDSLKGR-----RGRLPSKPKSPLQQEPSQPSPPSPPICMMNALVRALTD- 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 KREAVQEERQRGKDKDGDGECAGGAPEE-------MPVDRILEAELAVEQKSDQ 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10 GVEGPGGTGGSGSPND-----PVTNICQAAD----KQLFTLV-----EWAKRIP 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               457 GFTDLPKEDQTLLIESAFLELFVLRLSIRSNTAEDKFVFCNGLVLHRLQC-LRGFGEWLD 515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.9%; Score 530.5; DB 3; 29.2%; Pred. No. 1.1e-32; tive 68; Mismatches 187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; LOCATION: (292)..(523)
; OTHER INFORMATION: minimal ligand binding domain
US-08-980-115-7
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  Application US/08980115
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Best Local Similarity 29.2%
Matches 150; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 KAVPTVAGARFPLFHFKPSPPHPPAPSPAGGHHLGYDPTAAAALSLPLGAAAAAGSQAAA 237
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                                                                             APPLICANT: LEID, MARK
APPLICANT: KASTNER, PHILIPPE
APPLICANT: CHAMBON, PIERE,
TITLE OF INVENTION: PROTEINS, GENES ENCODING SAME, AND USAGE THEREOF
TOWNERS OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P--PPPLGSPFPVISSSMGSPGLPPPAPPGFSGPVSSPQINSTVSLPGGGSG----
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                                                                                                                                                                                                                                                                                 ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue NW Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CUCRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/216,592A
FILING DATE: 23-MR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/825,667
FILING DATE: 24-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: GOLDSTEIN, JORGE A
REGISTRATION NUMBER: 29,021
RRFERENCE/DOCKET NUMBER: 1383.0060002
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
; Sequence 4, Application US/08216592A; Patent No. 6635429
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
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Sequence 11572, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION:

POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT PELING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

SEQ ID NOS: 207012

SOCTWARE: PASESEQ for Windows Version 4.0

LENGTH: 577
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                                                                                                                                                                        118 PPASSPEDEVLPSTSMYFKQSPPSTPTTPAFPPQAGALWDEALPSAPGCIAPGPLLDPPM 177
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                                                            PKEDQTLLIESAPLELFVLRLSIRSNTAEDKFVFCNGLVLHRLQC-LRGFGEWLDSI-KD 519
                                                                                                                                                  520 FSLNLQSLNLDIQALACLSALSMIT-ERHGLKEPKRVEELCNKITSSLKDH-QSKGQALE 577
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165 P--PPPLGSPFPVISSSMGSPGLPPPAPPGFSGPVSSPQINSTVSLPGGSG-----
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                                                                                                                                                                                                                                 578 PTESKVLGALVELRKICTLGLORIFYLKL 606
                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 29.49
Matches 151; Conservative
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; ORGANISM: Human
US-09-949-016-11572
                                                                                                                                                                                                                                                                                                                                               RESULT 15
US-09-949-016-11572
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LENGTH: 626
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Sequence 14, App
                                                        March 12, 2005, 17:51:17; Search time 139 Seconds (without alignments) 1485.488 Million cell updates/sec
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Sequence 60, Appli
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Sequence 76, Appl
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Sequence 40, Appl
Sequence 82, Appl
Sequence 97, Appl
Sequence 34, Appl
Sequence 34, Appl
Sequence 76, Appl
    US-09-853-386-67

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US-09-853-386-69

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US-09-853-386-41

US-09-853-386-41

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US-10-205-951-81

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ALIGNMENTS

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Sequence 64, Application US/09853386

Sequence 64, Application US/09853386

Patent No. US2002043151A1

GENERAL INFORMATION:
APPLICANT: Murphy, Evelyn
APPLICANT: Conneely, Orla
APPLICANT: Conneely, Orla
APPLICANT: Conneely, Orla
FILE OF INVENTION: Subfamily of Nuclear Transcription Factors
TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors
FILE REFERENCE: POLYON NUMBER: US/09/853,386
CURRENT PILING DATE: 2001-05-11
FRIOR PILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 153
SOFTWARE: Patentin version 3.1
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99.9%; Score 3333; DB 9; Length 626;
Best Local Similarity 99.8%; Pred. No. 3.5e-217;
Matches 625; Conservative 0; Mismatches 1; Indels
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APPLICANT: Murphy, Evelyn
APPLICANT: Murphy, Evelyn
APPLICANT: Murphy, Evelyn
APPLICANT: Bresnihan, Barry
APPLICANT: Conneely, Orlea
APPLICANT: Fitzgerald, Oliver
TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR
TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors
TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors
TILE REFERENCE: P01972US1
CURRENT APPLICATION NUMBER: US /09/853,386
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/203645
PRIOR APPLICATION NUMBER: US 60/203645
NUMBER OF SEQ ID NOS: 153
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99.4%; Pred. No. 5e-216;
tive 1; Mismatches 3;
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Best Local Similarity 99.4<sup>3</sup>
Matches 622; Conservative
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; ORGANISM: HUMAN
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        SSPEDEVLPSTSMYFKQSPPSTPTTPAFPPQAGALWDEALPSAPGCIAPGPLLDPPMKAV 180
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FUDILication No. US2033220288A1
GENERAL INFORMATION.
APPLICANT: MILLIAN, SHANNON E.
APPLICANT: CONNEELY, ORLA M.
APPLICANT: CONNEELY, ORLA M.
TITLE OF INVENTION: AND THERAPY
TITLE OF INVENTION: AND TEFREY
TITLE OF INVENTION: AND TEFREY
TITLE OF INVENTION: AND TERMEN THERAPY
FILE REPRENCE: PO2454U1
CURRENT APPLICATION NUMBER: US/10/414,080
CURRENT PILING DATE: 2003-04-15
FRIOR APPLICATION NUMBER: 60/373,238
FRIOR APPLICATION NUMBER: 60/373,238
SPRIOR PILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 36
SSEQ ID NO 14
LENGTH: 626
                                                                                              HPYGLPLAKRAAPLAFPPLGLTPSPTASSLLGESPSLPSPPSRSSSSGEGTCAVCGDNAA
                                                                                                                                                                  HPYGLPLAKRAAPLAFPPLGLTPSPTASSLLGESPSLPSPPSRSSSSGEGTCAVCGDNAA
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Pred. No. 3.5e-217;
0; Mismatches 1;
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Best Local Similarity 99.8%;
Matches 625; Conservative (
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US-10-414-080-14
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US-10-414-080-14
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Publication No. US20050048507A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Sequence 96, Application US/09853386

Sequence 96, US20020049151A1

GENERAL INFORMATION:
APPLICANT: Murphy, Evelyn
APPLICANT: Conneely, Orla
APPLICANT: Fitzgerald, Oliver
TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the NURR
TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors
FILE REFERENCE: P01972US1
CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: US 60/203645
PRIOR FILING DATE: 2000-05-12
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SOFWARE: Patentin version 3.1
SEQ ID NO 96
LENGTH: 626
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Publication No. US20030220288A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
MILLICAN:
MILLICAN:
MILBRANDT, JEFFREY
TITLE OF INVENTION: NOR-1 AND NUR77 NUCLEAR RECEPTORS AS TARGETS FOR TITLE OF INVENTION: ANTI-LEUKEMIA THERAPY
FILE REPERENCE: P02454US1
CURRENT APPLICATION NUMBER: US/10/414,080
CURRENT FILING DATE: 2003-04-15
PRIOR PILING DATE: 2002-04-17
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                              Length
                             Score 3299.5; DB 9; Length
Pred. No. 6.5e-215;
1; Mismatches 3; Indels
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SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 625
                                Query Match
Best Local Similarity 99.2
Matches 621; Conservative
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CAGANISM: Homo sapiens
US-10-414-080-13
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US-10-414-080-13
US-09-853-386-63
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| Batent No. US20020049151A1
| APPLICANT: Murphy, Evelyn
| APPLICANT: Bresnihan, Barry
| APPLICANT: Subfamily of Nuclear Transcription Factors
| TITLE OF INVENTION: Therapeutic Approaches to Diseases by Suppression of the No. FILE REFERENCE: 2001-05-11
| TITLE OF INVENTION NUMBER: US/09/853,386
| CURRENT APPLICATION NUMBER: US/09/853,386
| PRIOR FILING DATE: 2000-06-12
| PRIOR FILING DATE: 2000-06-12
| NUMBER OF SEQ ID NOS: 153
| SOFTWARE: PatentIn version 3.1
| SEQ ID NO 63
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                                  Score 3316; DB 17;
Pred. No. 5e-216;
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                                  99.4%;
                                Query Match
Best Local Similarity 99.4
Matches 622, Conservative
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ORGANISM: HUMAN
US-10-659-004-116
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61 FWEGYSSNYELKPSCLYQMQPSGPRPLIKMEEGRAHGYHHHHHHHHHHQQQQQQQP 120
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                                                                      1 MPCVQAQYSPSPPGSSYAAQTYSSEYTTEIMNPDYTKLTMDLGSTEITATATTSLPSIST
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                                       Gaps
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PUBLICATION NO. US20030220288A1

GENERAL INFORMATION:
APPLICANT: MULLICANY, SHANNON E.
APPLICANT: MILERANDT, JEFFREY
TITLE OF INVENTION: NOR-1 AND NUR77 NUCLEAR RECEPTORS AS TARGETS FOR TITLE OF INVENTION: ANTI-LEUKEMIA THERAPY
TITLE OF INVENTION: NOR-1 AND NUR77 NUCLEAR RECEPTORS AS TARGETS FOR TITLE OF INVENTION: NOWBER: US/10/414,080
CURRENT FILING DATE: 2003-04-15
PRIOR PILING DATE: 2002-04-17
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PATENTIN VOY: 2.1
SEQ ID NO 17
LENGTH: 643
                                     17;
   Length 643;

    Score 3133.5; DB 9; Length
    Pred. No. 1.2e-203;
    Mismatches 22; Indels

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     93.9%;
 Query Match
Best Local Similarity 92.4*
Matches 594; Conservative
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US-10-414-080-17
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US-10-414-080-17
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Facture No. US20020049151A1

Facture No. US20020049151A1

GENERAL INFORMATION:

APPLICANT: MITCHING Barry

APPLICANT: Conneely, Orla

TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors

TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors

FILE REFERENCE: P01972US1

CURRENT FILING DATE: 2001-05-11

PRIOR APPLICATION NUMBER: US 60/203645

FRICH REPERSON OF SEQ ID NOS: 153

SOFTWARE: Patentin Version 3.1

FROM FILING DATE: 2001-05-12

NUMBER OF SEQ ID NOS: 153

SOFTWARE: Patentin Version 3.1
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Score 3299.5; DB 15; Length 625; Pred. No. 6.5e-215; 1; Mismatches 3; Indels 1;
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   98.9%;
Query Match 98.9
Best Local Similarity 99.2
Matches 621; Conservative
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; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-853-386-70
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US-09-853-386-70
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Best Local Similarity 92.2
Matches 582; Conservative
     Best Local Similarity 99.8
Matches 586; Conservative
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Publication No. US20040171823A1

GENERAL INFORMATION

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: PATHWAY

TITLE OF INVENTION: PATHWAY

TITLE OF INVENTION: PATHWAY

CURRENT APPLICATION NUMBER: US/10/755,889

CURRENT FILING DATE: 2004-01-13

PRIOR PELICATION NUMBER: U.S. 60/440,068

PRIOR APPLICATION NUMBER: U.S. 60/440,068

PRIOR PELING DATE: 2003-01-14

PRIOR PILING DATE: 2003-01-14

PRIOR FILING DATE: 2003-05-12

NUMBER OF SEQ ID NOS: 823

SOFTWARE: PATENTING DATE: 2003-05-12

SEQ ID NOS: 823

LENGTH: 587
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                                                          1 MPCVQAQYSPSPPGSSYAAQTYSSEYTTEIMNPDYTKLTMDLGSTEITATATTSLPSIST
                                                                          FVEGYSSNYELKPSCVYQMQ----RPLIKVEEGRAPSYHHHHHHHHHHHQQ-----
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                                  Gaps
                                17;
       DB 15; Length 643;
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                                  22; Indels
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     tch 93.9%; Score 3133.5; DB 1 al Similarity 92.4%; Pred. No. 1.2e-203; 594; Conservative 10; Mismatches 22;
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Query Match
Best Local Similarity
Matches 594; Conserv
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US-10-755-889-64
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Query Match

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APPLICANT: Murphy, Evelyn
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APPLICANT: Murphy, Evelyn
APPLICANT: Bresnihan, Barry
APPLICANT: Conneally, Oxla
APPLICANT: Fitzgerald, Oliver
TITLE CONNEWITON: Therapeutic Approaches to Diseases by Suppression of the NURR
TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors
TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors
FILE REFERENCE: PO1972US1
CURRENT APPLICATION NUMBER: US/09/853,386
CURRENT APPLICATION NUMBER: US 60/203645
PRIOR FILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 153
SOFTWARE: Patentin version 3.1
SEQ ID NO 66
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92.2%; Pred. No. 1.2e-199;
iive 12; Mismatches 29;
Pred. No. 5.3e-203;
                 0; Mismatches
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us-10-608-863-2.rapb

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APPLICANT: Murphy, Evelyn
APPLICANT: Murphy, Evelyn
APPLICANT: Eresnihan, Barry
APPLICANT: Conneely, Orlver
TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors
CURRENT APPLICATION NUMBER: US/09/853,386
CURRENT FILING DATE: 2001-05-11
PRIOR PILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 153
SUFTWARE: Patentin Version 3.1
SEQ ID NO 73
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IPPASSPEDEVLPSTSMYFKQSPPSTPTTPAFPPQAGALWDEALPSAPGCIAPGPLLDPP
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Pred. No. 1.2e-199;
2; Mismatches 29;
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APPLICANT: Murphy, Evelyn
APPLICANT: Murphy, Evelyn
APPLICANT: Comneely, Orly
APPLICANT: Comneely, Orly
APPLICANT: Comneely, Orly
APPLICANT: Fitzgerald, Oliver
TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors
TITLE OF INVENTION: Subfamily of Nuclear Transcription Factors
FILE REPERRICE: P019720S1
CURRENT APPLICATION NUMBER: US/09/853,386
CURRENT APPLICATION NUMBER: US 60/203645
PRIOR APPLICATION NUMBER: US 60/203645
PRIOR PILING DATE: 2000-05-12
NUMBER OF SEQ ID NOS: 153
SOFTWARE: Patentin version 3.1
SEQ ID NO 68
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1 MPCVQAQXSPSPPGSTYATQTYGSEYTTEIMNPDYAKLTMDLGSTGIMATATTSLPSFST
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; Sequence 68, Application US/09853386
; Patent No. US20020049151A1
; GENERAL INFORMATION:
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Matches 582; Conservative
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FVEGYSSNYELKPSCVYOM----ORPLIKVEEGRAPSYHHHHHHHHHHHQQQHQQPS
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US-10-414-080-15
is Sequence 15, Application US/10414080
; Publication No. US20030220288A1
; GENERAL INFORMATION:
; APPLICANT: MULLICAN', SHANNON E.
; APPLICANT: MILBRANDT, JEFFREY
; TITLE OF INVENTION: ANTI-LEUKEMIA THERAPY
; TITLE OF INVENTION: ANTI-LEUKEMIA THERAPY
; FILE REPERENCE: PO2454U81
; CURRENT APPLICATION NUMBER: US/10/414,080
; CURRENT FILING DATE: 2003-04-15
; FRIOR APPLICATION NUMBER: 60/373,238
; FRIOR FILING DATE: 2002-04-17
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SOFTWARE: Patentin Ver. 2..;
SEQ ID NO 15
LENGTH: 628
TYPE: PRT
CRGANISM: RAT
US-10-414-080-15
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                                                                                                                                                 119 IPPPSGPEDEVLPSTSMYFKQSPPSTPTTPGFPPQAGALWDDELPSAPGCIAPGPLDPQ 178
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FVEGYSSNYELKPSCVYQM----QRPLIKVEEGRAPSYHHHHHHHHHHHQQQHQQPS
                                                                            179 MKAVPPMAAARFPIF-FKPSPPHPPAPSPAGGHHLGYDPTAAAALSLPLGAAAAAGSQA
                                                                                                                                                                                                                                                                                                       238 AALEGHPYGLPLAKRTATLTFPPLGLTASPTASSLLGESPSLPSPPNRSSSSGEGTCAVC
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; Sequence 4, Application US/10005169
; Publication No. US20020152492A1
; GENERAL INFORMATION:
    APPLICANT: Guenther, Catherine
; APPLICANT: Allen, Keith D.
; TITLE OF INVENTION: TRANSGENIC MICE CONTAINING NOR1 GENE
; TITLE OF INVENTION: DISRUPTIONS
; FILE REFREENCE: R-687
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: US 60/251,794
; PRIOR APPLICATION NUMBER: US 60/251,794
; PRIOR APPLICATION NUMBER: US 60/324,614
; PRIOR PLING DATE: 2000-12-06
; PRIOR PLING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FABLSEQ for Windows Version 4.0
; SEQ ID NOS: 6
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Search completed: March 12, 2005, 18:03:55 Job time : 141 secs

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                                                                                                        March 12, 2005, 17:41:22 ; Search time 42 Seconds
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ALIGNMENTS

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A,Map position: 9q
C;Superfamily: probable hormone receptor N10, nuclear; erbA transforming protein homolocisuperfamily: probable hormone receptor N10, nuclear; erbA transforming protein homology c,Reywords. DNA binding; receptor; zinc finger
F;290-377/Domain: erbA transforming protein homology c,RBA>
F;290-377/Domain: DNA binding #status predicted c,DNA>
F;292-312/Region: zinc finger CCCC motif
F;310-314/Region: zinc finger CCCC motif
F;328-352/Region: zinc finger CCCC motif
F;329-333/Region: D box
F;310-316/Region: A box
                                                                                                                                  Rjohkura, N.; Ito, M.; Tsukada, T.; Sasaki, K.; Yamaguchi, K.; Miki, K.
Biochim. Biophys. Acta 1108, 205-214, 1996
A;Title: Structure, mapping and expression of a human NOR-1 gene, the third member of
A;Reference number: S71930; MUID:96404972; PMID:8809112
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                                                               C;Species: Homo sapiens (man)
C;Date: 04-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 20-Feb-1998
C;Accession: S71930
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99.2%; Pred. No. 4.8e-174;
ive 1; Mismatches 3;
                                              neuron-derived receptor NOR-1 - human
                                                                                                                                                                                                                               A,Accession: S71930
A,Molecule type: mRNA
A,Residues: 1-625 <OHK>
A,Cross-references: EMBL:D78579
A,Note: DNA was also sequenced
C;Genetics:
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Matches 621; Conservative
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neuron-derived receptor NOR-2 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 16-Aug-2004
C;Accession: S66671
EFBS Lett. 372, 273-278, 1995
A;Title: NOR-2 (neuron-derived orphan receptor), a brain zinc finger protein, is laterance number: S66671; MUID:96000221; PMID:755683
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               GDNAACQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCPVDKRRNRCQYCRFQKCLSV
                                                                                                                          YSRYCPTDQAAAGTDAEHVQQFYNLLTASIDVSRSWAEKIPGFTDLPKEDQTLLIESAFL
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                                                                             GDNAACQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCPVDKRRNRCQYCRFQKCLSV
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89.6%; Pred. No. 1.3e-104;
iive 10; Mismatches 26;
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Matches 379; Conservative
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361 VVRTDSLKGRRGRLPSKPKSPLQQEPSQPSPPICMMNALVRALTDSTPRDLDYSRYC
                                                                       RISIRSNTAEDKFVFCNGLVLHRLOCLRGFGEWLDSIKDFSLNLOSLNLDIQALACLSAL
                                                                                                           480 RISIRSNTAEDKFVFCNGLVLHRLQCLRGFGEWLDSIKDFSLNLDQSLNLDIQALAÇLSAL
                                                                                                                                             SMITERHGLKEPKRVEELCHKITSSLKDHQSKGQALEPNESKVLVALVELRKICTLGLQR
                           VVRTDSLKGRRGRLPSKPKSPLQQEPSQPSPPSPPICMMNALVRALTDSTPRDLDYSRYC
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llarity 92.2%; Pred. No. 1.2e-161;
Conservative 12; Mismatches 29;
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QY 117 IPPASSPEDEVLPSTSMYFKQSPPSTPTTPAFPPQAGALMDEALPSAPGCIAPGPLLDPP 176 Db 119 IPPPSGPEDEVLPSTSMYFKQSPPSTPTTPGFPPQAGALMDDELPSAPGCIAPGPLLDPQ 178	کن م	172 LLDPPMKAVPTVAGARFPLFHFKPSPPHPPA
OY 177 MKAVPTV-AGARFPLFHFKPSPPHPPAPSPAGGHLGYDPTAAAALSLPLGAAAAAGSQA 235	ò a	208 GHHLGYDPTAAAALSLPLGAAAAGSQAALESHPYGLP-LAKRAAPLAFPPLGLTPSPT 266
Qy 236 AALESHPYGLPLAKRAAPLAFPLGLTPSPTASSLLGESPSLPSPFSRSSSGGGTCAVC 295 Db 238 AALEGHPYGLPLAKRTATLTFPPLGLTASPTASSLLGESPSLPSPPNRSSSGGGTCAVC 297	ò 8	267 ASSLLGESPSLPSPPSRSSSGEGTCAVCGDNAACQHYGVRTCEGCKGFFKRTVQKNAKY 326
Qy 296 GDNAACQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCPVDKRRRNRCQYCRFQKCLSV 355 Db 298 GDNAACQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCPVDKRRRNRCQYCRFQKCLSV 357	<i>장</i> 점	327 VCLANKNCPVDKRRRNRCQYCRFQKCLSVGMVKEVVRTDSLKGRRGRLPSKPKSPLQQEP 386
Qy 356 GWVKEVVRTDSLKGRRGRLPSKPKSPLQQEPSQPSPPSPPICMMALVRALTDSTPRDLD 415 Db 358 GWVKEVVRTDSLKGRRGRLPSKPKSPLQQEPSQPSPPSPPICMMNALVRALTDATPRDLD 417	& a	387 SQPSPPSPPIÇMMNALVRALTDSTPRDLDYSRY-CPTDQAAAGTDAEHVQQFYNLLTA 443
Oy 416 YSR 418 	& qa	444 SIDVSRSWAEKIPGFTDLPKEDQTLLIESAFLELFVLRLSIRSNTAEDKFVFCNGLVLHR 503
RESULT 4 A57040 T cell nuclear receptor NOT - human	S & &	LQCLRGFGEWLDSIKDFSLNLQSLNLDIQALACLSALSMITERHGLKEPKRVEELCNKIT
C.breites: nome sapiens mann C.breites: nome C.breites: nome 0.5004 C.breites O.S.cot-1995 #sequence revision 0.50ct-1995 #sequence C.breites: 0.50ct-1995 F. Breites: 0.50ct-19	3 € €	564 SSLKHRQSKUQALETIE-SKVLGALVELKKICTIGLQKIFYLKLEDLVSFPSIIDKLF 620
Mol. Endocrinol. 8, 1583-1591, 1994 A;Title: NOT, a human immediate-early response gene closely related to the steroid/thyro A;Reference number: A57040; MUID:95183071; PMID:7877627 A;Accession: A57040	· 6	621 LDTLPF 626 593 LDTLPF 598
A;Status: preliminary A;Molecule type: mRNA A;Residues: 1-598 cMG>	RESULT	
A,Cross-references: UNIPROT:P43354; EMBL:X75918; NID:g415822; PIDN:CAA53518.1; PID:g4158 R;Okabe, T.; Takayanagi, R.; Imasaki, K.; Haji, M.; Nawata, H.; Watanabe, T. J. Timunol. 154, 3811-3879, 1995 A;Title: cDNA cloning of a NGFI-B/nur77-related transcription factor from an apoptotic h	. w	nuclear orphan receptor Nurrl - mouse N'Alternate names: Nur-related transcription factor 1 C'Species: Mus musculus (house mouse) C'Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
A; Reference number: 156260; MUID: 95221892; PMID: 7706727 A; Accession: 156260 A; Status: preliminary; translated from GB/EMBL/DDBJ	C; Acces R; Law, Mol. En	sion: A46225 3.W.; Conneely, O.M.; DeMayo, F.J.; O'Malley, B.W. locrinol. 6, 2129-2135, 1992
A;MOLECULE LYPE: HEARA A;Residues: 64-464, W',466-467, W',469-598 <res> A;Cornest references: GB:S77154; NID:g913966; PIDN:AAB33999.1; PID:g913967 C:Gonestics:</res>	A; Iltie A; Refer A; Acces	: Identification of a new brain-specific transcription factor, Nukki sico: A46225; MUID:93149122; PMID:1491694 sico: A46225.
A;Gene: GDB:NURR; TINUR; NOT A;Cross-references: GDB:624567; OMIM:601828 A;Map position: 2q22-2q23		s: prefilminary leb type: nucleic acid nes: 1-598 <law> -references: UNIPROT:Q06219; GB:S53744; NID:g264410; PIDN:AAB25138.1; PID:g26441</law>
C;Superiamily: probable normone receptor N10, nuclear; erbA transforming protein homolog C;Keywords: DNA binding; zinc finger F;261-514/Domain: erbA transforming protein homology <erba></erba>		<pre>imental source: brain sequence extracted from NCBI backbone (NCBIN:123734, NCBIP:123736) family: probable hormone receptor N10, nuclear; erbA transforming protein homolo- da: DNA binding: nuclear; transcription requiation; zing finger</pre>
52.5%; Score 1751; DB 2; Length 598; Larity 54.5%; Pred. No. 4.76-89;	F;261-5	4/Domain: erbA transforming protein homology < ERBA>
Maccnes 363; Conservative 74; Mismatches 121; Indels 108; Gaps 18; Qy	Query M Best Lo Matches	Query Match 52.3%; Score 1746; DB 2; Length 598; Best Local Similarity 54.4%; Pred. No. 8.8e-89; Matches 362; Conservative 75; Mismatches 121; Indels 108; Gaps 18;
Db 1 MPCVQAQYGSSPQGASPASGSYHSGERYSSDFLTPEFVKFSMDLTWTEL-TATTSLP 58 Qy 57 SISTFVEGYSSNYELKPSCVYQMQRPLIKVEEGRAPSYHHHHHHHHHHHHHHHQQQH 112	& a	1 MPCVQAQXSPSPPGSSYAAQTYSSEYTTEIMNPDYTKLTMDLGSTEITATATTSLP 56
Db 59 SFSTFMDNYSTGYDVKPPCLYQMPLSGQQSSIKVEDIQMHNYQQHSH 105	ð 1	57 SISTEVEGYSSNYELKPSCVYQMQRPLIKVEEGRAPSYHHHHHHHHHHHHHHHHHHQQQH 112
	G &	LPSAPGCIAPGP

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74;
54.1%;
            Conservative
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A; Residues: 1-598 <NAK>
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A;Molecule type: mRNA
A;Residues: 1-598 <PEN>
A;Residues: 1-598 <PEN>
A;Cross-references: UNPROT: 007917; EMBL: U01146; NID: 9515968; PIDN: AAC52143.1; PID: 95415
A;Cross-references: UN-Y: Laz, T.M.; Hazel, T.G.; Lau, L.F.; Taub, R.
J. Biol. Chem. 268, 8855-8861, 1993
A;Title: RNR-1, a nuclear receptor in the NGFI-B/Nur77 family that is rapidly induced in
A;Reference number: A46050; MUID: 93232045; PMID: 8473329
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C;Superfamily: probable hormone receptor N10, nuclear; erbA transforming protein homolog
C;Keywords: DNA binding; nucleus; steroid hormone receptor; transcription regulation; zi
F;261-514/Domain: erbA transforming protein homology <BRBA>
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                                                                                                                                                                                                                                                                      443
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                                                                                                                                                                                                                                                                                       353 QDPSPPSPPVSLISALVRAHVDSNPAMTSLDXSRPQANPDYQMSGDDTQHIQQFYDLLTG
                                                                                                                                                                                                                                                                                                                                                 --PGS
                                -- PSPAG
                                                              LHNFHQNYVATTHMIBQRKTPVSRLSLFSFKQSPPGTPVSSCQMRFDGPLHVPMNPEPAG
                                                                                          GHHLGYDPTAAAALSLPLGAAAAGSQAAALESHPYGLP-LAKRAAPLAFPPLGLTPSPT
                                                                                                             ASSLLGESPSLPSPPSRSSSGEGTCAVCGDNAACQHYGVRTCEGCKGFFKRTVQKNAKY
                                                                                                                                                                               240 ASQLL--DIQVPSPPSRGSPSNEGLCAVCGDNAACQHYGVRTCEGCKGFFKRTVQKNAKY
                                                                                                                                                                                                              VCLANKNCPVDKRRRNRCQYCRFQKCLSVGMVKEVVRTDSLKGRRGRLPSKPKSPLQQEP
                                                                                                                                                                                                                              SQPSPPSPPICMMNALVRALTDSTP--RDLDYSRY-CPTDQAAAGTDAEHVQOFYNLLTA
                                                                                                                                                                                                                                                                                                                                SIDVSRSWAEKIPGFTDLPKEDQTLLIESAFLELFVLRLSIRSNTAEDKFVFCNGLVLHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                     564 SSLKDHQ--SKGQALEPTE-SKVLGALVELRKICTLGLQRIFYLKLEDLVSPPSIIDKLF
   ----LPPQS----EEMMPHSGSVYYKPSSPPTPSTPSFQVQHSPMWDD-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cispecies: Rattus norvegicus (Norway rat)
Cibate: 02-Mug-1996 #sequence_revision 02-Aug-1996 #text_chacibace: 02-Aug-1996 #text_chacibacesion: 184692; AaGo500
Ripena de Ortiz, S.; Cannon, M.M.; Jamieson, G.A.
Brain Res, Mol. Brain Res. 23, 278-283, 1994
A;Title: Expression of nuclear hormone receptors within the A;Reference number: 148178; MUID:94335560; PMID:7914660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nuclear orphan receptor HZF-3 - rat
N;Alternate names: thyroid/steroid receptor homolog RNR-1
                                ----VAGARFPLFHFKPSPPHPPA
                                                                                                                           209 SHHV-----
                                  LLDPPMKAVPT
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Residues: 1-181,'A'
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Length 598;

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stern NAIDabble nuclear hormone receptor ST-59; stern NAIDabble nuclear hormone receptor ST-59; stern NAIDabble nuclear Homo sapiens (man) c; species: Homo sapiens (man) c; species: Homo sapiens (man) c; species: 28-mar-1991 #sequence revision 28-Mar-1991 #text_change 09-Jul-2004 c; pate: 28-mar-1991 #sequence revision 28-Mar-1991 #text_change 09-Jul-2004 c; pate: 28-mar-1991 #sequence revision A3121; A138-1443, 1990 A; Tible: A human early response gene homologous to murine nur77 and rat NGFI-B, and A; Arcession: A37251; MUID:91133413; PMID:2283997 A; A; Azcession: A37251                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: UNIPROT: P22736; GB: D49728; NID: G1813881; PIDN: BAA08565.1; A; Note: it is uncertain whether Met-1 or Met-35 is the initiator R; Bondy, G.P. R; Bondy, G.P. Cell Growth Differ. 2, 203-208; 1991 A; Title: Phorbol ester, forskolin, and serum induction of a human colon nuclear A; Reference number: A61191; MUID: 91329278; PMID: 1651101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          298 VCLANKNCPVDKRRRNRCQYCRFQKCLAVGMVKEVVRTDSLKGRRGRLPSKPKS----P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQPSPPSPPICMMMALVRALTDSTP--RDLDYSRY-CPTDQAAAGTDAEHVQQFYNLLTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASSLLGESPSLPSPPSRSSSGEGTCAVCGDNAACQHYGVRTCEGCKGFFKRTVQKNAKY
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                                                                                                                                                                                                                                                                SISTFVEGYSSNYELKPSCVYOM----ORPLIKVEEGRAPSYHHHHHHHHHHHHQQQH
                                                                                                                                                                                                                                                                                                                                                                                                                113 QQPSIPPASSPEDEVLP-STSMYFKQSPPSTPTTPAFPPQAGALWDEALPSAPGCIAPGP
                                                                                                        ---SSEYTTEIMNPDYTKLTMDLGSTEITATATTSLP
                                                                                                                                                108;
                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLDPPMKAVPT-----VAGARFPLFHFKPSPFHPPA--
Pred. No. 8.6e-88;
1; Mismatches 124;
                                                                                                                MPCVQAQYSPSPPGSSYAAQTY
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Accession: S33763

hormone receptor NGFI-B homolog - African clawed frog

hormone receptor NGFI-B homolog - African clawed frog

C.Species Xenopus laevis (African clawed frog)

C.Species S33763; S31713

C.Accession: S33763; B31713

C.Accession: S33763; S31713

S.Accession: S33763; S31713

A.Title: Cloning and sequencing of a Xenopus homologue of the inducible orphan receptor A.Title: Cloning and sequencing of a Xenopus homologue of the inducible orphan receptor A.Title: Cloning and sequencing of a Xenopus homologue of the inducible orphan receptor A.Title: Cloning and sequencing of a Xenopus homologue of the inducible orphan receptor A.Title: Cloning and sequencing of a Xenopus homologues

A.Accession: S33763

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117 IPPAS--SPEDEVLPSTSMYPKOSPPS--TPTTPAFPPOAGALWDEALPSAPGCIAPGPL 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LDP----PMKAVPTVAGARFPLFHFKPSPPHPPAPSPAGGHHLGYDPTAAALSLPLGAA 228
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probable hormone receptor N10, nuclear - mouse
N/Alternate names: steroid hormone receptor homolog nur/77
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 CYPGSFTNQLDETMSSSGSDYYGSPCSIPSPSTPGFQNPQLPTWE----CSYGAYSPTQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVDTDVFALAQNSSAGFPAV-----PLGQAPGVLDSSVLLDSPLSPS-KTRSPSSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 YDNMRHWTEQOKNSISQOTF--FSF-GTPAHSP-----NMAANPLKIAPATHRLDQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              414 QDLLLESAFLELFILRLAYRSRPEEGKLIFCNGVVLHRTQCVRGFGEWIDSIIEFSHSLQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MPCVQAQYSPSPPGSSYAAQTYSSEYTTEIMNPDYTKLTMDLGSTEITATATTSLPSIST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      577;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40.5%; Score 1350.5; DB 2; Length
47.1%; Pred. No. 4.4e-67;
ive 88; Mismatches 162; Indels
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A;Accession: A61191
A;Accession: A61191
A;Molecule type: mRNA
A;Residues: 35-252, 1',254-598 <BON>
R;Chang, C.; Kokontis, J.; Liao, S.; Chang, Y.
S. Steroid Biochem. 34, 391-395, 1989
A;Title: Isolation and characterization of human TR3 receptor: a member of steroid receptors of the special problem. A61451
A;Reference number: A61451; MUID:90173205; PMID:2626032
A;Recession: A61451
A;Residues: 1-261, P', 263-369, 'L', 371-598 <CHA>
A;Residues: 1-261, 'P', 263-369, 'L', 371-598 <CHA>
A;Gene: GDB:HMR
A;Gene: GDB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41.0%; Score 1367; DB 2; 47.5%; Pred. No. 5.7e-68;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 47.5'
Matches 317; Conservative
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oA transforming protein homolog, transcription regulation; zinc
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A;Residues: 1-563 <MIL>
A;Cross-references: GB:U17254; NID:g596053; PIDN:AAA56770.1; PID:g596054
A;Experimental source: cell line PC12
B;Matson, M.A.; Milbrandt, J.
Mol. Cell. Biol. 9, 4213-4219, 1989
A;Title: The NGFI-B gene, a transcriptionally inducible member of the steroid receptor A;Reference number: A34097; MUID:90066426; PMID:2479823
A;Reference number: A34097
A;Residues: preliminary
A;Wolecule type: DNA
A;Residues: 255-260;298-303;349-354;417-422;476-481 <WAT>
C;Comment: This protein is proposed to be a ligand-dependent transcriptional activator of the steroid retranscriptional activator of the steroid receptor of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       to the glucocorticoid receptor
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                                                                                                                                                                                                                                              nerve growth factor-inducible protein B - rat
N'Alternate names: glucocorticoid receptor homolog
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Aug-1999
C;Accession: JQ0623; A34097
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C;Superfamily: probable hormone receptor N10, nuclear; erbA transforming
C;Keywords: DNA binding; growth factor receptor; nucleus; transcription r
F;230-479/Domain: erbA transforming protein homology <ERBA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Néuron 1, 183-188, 1988
A,Title: Nerve growth factor induces a gene homologous t
A,Reference number: JQ0623; MUID:90166506; PMID:3272167
A,Accession: JQ0623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38.3%; Score 1277; DB 2; 146.6%; Pred. No. 4.7e-63; Partive 70; Mismatches 145;
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                                                                                                                                          A; Accession: S06953
A; Molecule type: DNA
A; Residues: 1-601 «RYS
A; Residues: 1-601 «RYS
A; Residues: UNIPROT: P12813; EMBL: X16995; NID: 953312; PIDN: CAA34862.1; PID: 953313
A; Residues: UNIPROT: P12813; EMBL: X16995; NID: 953312; PIDN: CAA34862.1; PID: 953313
B; Hazel, T.G.; Nathans, D.; Lau, L.F.
B; Reference number: A94211; MUID: 89042200; PMID: 3186734
A; Reference number: A94211; MUID: 89042200; PMID: 3186734
A; Residues: L. 601 «HAZ»
A; Roberoule type: MRNA
A; Residues: L. 601 «HAZ»
A; Conserreferences: GB:J04113; NID: 9200115; PIDN: AAA39843.1; PID: 9200116
C; Genetics: L. 602 (A) 3391; 389/3; 457/2; 517/1
C; Superfamily: probable hormone receptor N10, nuclear; erbA transforming protein homology (ERBA)
E; 266-517/Domain: erbA transforming protein homology (ERBA)
F; 270-280/Region: zinc finger CCCC motif
F; 306-330/Region: zinc finger CCCC motif
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                                                                                           A,Title: Structure, mapping and expression of a growth factor inducible gene encoding A,Reference number: S06953; MUID:90059925; PMID:2555161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               348 RRGRLPSKPKQP------PDASPTNLLTSLIRAHLDSGPSTAKLDYSKFQELVLPRF 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGLKEPKRVEELCNKITSSLKDHQSKGQALEPTE----SKVLGALVELRKICTLGLQRIF 602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       56 PSISTFVEGYSSNYELKPSCVYOM --- ORPLIKVEEGRAPSYHHHHHHHHHHHHHHHQQQH 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --EALPSAPGCIAPGPLLDPPMKAVPTVAGARFPLFH 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              152 QLSPWDGSFGHFSPSQTYEGLWAWTEQLPKA---SSGP---PP-----PPTF 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FKPSPPHPPAPSPAGGHHLGYDPTAAALSLPLGAAAAGSQAAALESHPYGLPLAKRAA 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rsrspprgpspslagsslklfpppathQlg------229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   487 NTAEDKFVFCNGLVLHRLQCLRGFGEWLDSIKDFSLNLQSLNLDIQALACLSALSMITER 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113 QQPSIPPASS-----TPTTPAFPPQ 151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20
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                                  s:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Accession: 806953; A30059; A31344; Ryseck, R.P.; Macdonald-Bravo, H.; Mattei, M.G.; Ruppert, MBO J. 8, 3327-3335, 1989
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Matches 307; Conservative
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DHR38 protein - silkworm (fragment)
C;Species: Bombyx mori (silkworm)
C;Species: Bombyx mori (silkworm)
C;Species: Bombyx mori (silkworm)
C;Date: l3-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 16-Aug-2004
C;Accession: S58205
R;Sutherland, J:; Kozlova, T:; Tzertzinis, G:; Kafatos, F.C.
A;Bescription: DHR38: a new partner for USP suggests an unexpected role for NGFI-B type
A;Recession: S58205
A;Accession: S58205
A;Accession: S58205
A;Accession: S58205
A;Accession: SF8205

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N;Alternate names: protein C48D5.1; steroid hormone receptor family member CNR8
C;Species: Caenorhabditis elegans
C;Date: 03.Mar-2000 #sequence_revision 03-Mar-2000 #text_change 09-Jul-2004
C;Accession: T43348; T20039; T45068
R;Sluder, A.E.; Mathews, S.W.; Hough, D.; Yin, V.P.; Maina, C.V.
Genome Res. 9, 103-120, 1999
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; Pred. No. 2.6e-49;
47; Mismatches 95; Indels 14;
                                                                                                                                                                                                                                                          574 QALEPTESKVIGALVELRKICTLGLORIFYLKLEDLVSPPSIIDKLFLDTLPF
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Best Local Similarity 57.4%;
Matches 210; Conservative 4'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DHRAB protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Species: 13-5an-1996 #sequence_revision 19-Apr-1996 #text_change 16-Aug-2004
C;Accession: S58238
R;Sutherland, J.; Kozlova, T.; Tzertzinis, G.; Kafatos, F.C.
submitted to the EMBL Data Library, June 1995
A;Bescription: DHR38: a new partner for USP suggests an unexpected role for NGFI
A;Accession: S58238
A;Conex: references: EMBL:X89246; NID:g929561; PIDN:CAA61534.1; PID:g929562
C;Genetics:
A;Gene: FlyBase:Hr38
A;Cross-references: FlyBase:FBgn0014859
C;Superfamily: erbA transforming protein homology
C;Keywords: zinc finger
F;220-467/Domain: erbA transforming protein homology
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                                                                                                                                                       ALACLSALSMITERHGLKEPKRVEELCNKITSSLKDHQSKGQALEPTE----SKVLGALV 588
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                             AFLELFVLRLSIRSNTAEDKFVFCNGLVLHRLQCLRGFGEWLDSIKDFSLNLQSLNLDIQ
                                                                 LPLGAAAAAGSQAAAL---ESHPYGLPLAKRAAPLAFPPLGLTPSPTASSLLGESPSLP
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                                                                                                                                                                                                                                                                                                                  ELRKICTLGLQRIFYLKLEDLVSPPSIIDKLFLDTLPF
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Title: The nuclear receptor superfamily has undergone extensive proliferation and diversence number: 222443; MUID:99148134; PMID:10022975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 16.6%; Score 554.5; DB 1; Length 619; Best Local Similarity 28.4%; Pred. No. 2.4e-23; Matches 190; Conservative 79; Mismatches 249; Indels 151.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 TMQAFQMPHNDLFLATAAPHYNPFALSNDFWPNPLMPSFTSPFYPQH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57 EMSKNSSCSSSFDYGEFGPSSSSRKGSKTTDADLDSL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 LODOFSNCSPAS -- VDSSYSSCSSVEDEIETYTRLVRN-
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CiAccession: G88408
Stanonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A;Root; MID:99066613; PMID:9881916
A;Noce: see websites genome.wustl.edu/gsc/C_elegans/ and www sanger.ac.uk/Projects/C_ele
A;Noce: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Map position: 3
C;Superfamily: Caenorhabditis elegans nuclear steroid hormone receptor NHR-6; erbA trans
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612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FVFCNGLVLHRLQCLRGFGE------WLDSIKDFSLNLQSLNLDIQALACLSALSMI- 543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           397 IMFESG----ELFSLNAFPACFQQIIRFMVDKARTFS---SLVDWEPQAFAAFIALQFLA 449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: G88408
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-562 <STO>
A;Residues: 1-562 <STO>
A;Residues: GB:Chr_III; PIDN:CAA85271.1; PID:g3875028; GSPDB:GN00021
                                                                                                                                                                                                                                                                                                                                                                                 protein nhr-6 [imported] - Caenorhabditis elegans
C,Species: Caenorhabditis elegans
C,Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 17-May-2002
                                                                                                                     105 HHHHQQQHQQPSIPPASSPEDEVLPSTSMYFKQSPPSTPTTPAFPPQAGALWDEALPSAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSLVETSDQVNTVPKPTKTEVESIPEE---FEOKPSSS------SHRLPSEM
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                                                                                 553 KRVEELCNKITSSLKDHQSKGQALEPTESKVLGALVELRKICTLGLQRIFYLKLEDLVSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16.6%; Score 554; DB 2; I
llarity 30.1%; Pred. No. 2.3e-23;
Conservative 72; Mismatches 199;
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SHQLPEEFM 579
                                                                                                                                                                                                   613 PSIIDKLFL 621
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Job time : 44 secs
                                                                                                                                                                                                                                                                                                   retinoic acid receptor beta-1 - chicken
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Accession: S13512; S17073
R;Padanilam, B.J.; Mcleod, L.B.; Suzuki, H.; Solursh, M.
Nucleic Acids Res. 19, 395, 1991
A;Title: Nucleotide sequence of an isoform of chicken retinoic acid binding protein-beta
A;Reference number: S13512; MUID:91195065; PMID:1849630
A;Coss-references: UNIPROT:P22448; EMBL:X56674; NID:g63785; PIDN:CAA39997.1; PID:g63786
A;Notes: the nucleotide sequence was submitted to the EMBL Data Library, November 1990
R;Notes: the nucleotide sequence was submitted to the EMBL Data Library, November 1990
B;Onhon, T: Muto, K: NO31, S:; Saito, T: Taniguchi, S.
B;Ochim. Biophys. Acta 1089, 273-275, 1991
A;Title: Isoforms of retinoic acid receptor beta expressed in the chicken embryo.
A;Reference number: S16243; MUID:91274365; PMID:1647216
A;Reference number: S16243; MUID:91274365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180 VPTVAGARFPLFHFKPSPPHPPAPSPAGGHHLGYDPTAAAALSLPLGAAAAAGSQAAALE 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               88 CFVCQDKSSGYHYGVSACEGCKGFFRRSIQKWMYTCHRDKNCVINKVTRNRCQYCRLQK 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             464 EDQTLLIESAFLELFVLRLSIRSNTAEDKFVFCNGLVLHRLQCLR-GFGEWLDSIKDFSL 522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                292 CAVCGDNAACQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCPVDKRRNRCQYCRFQK 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 352 CLSVGMVKEVVRTDSLKGRRGRLPSKPKSPLQQEPSQPSPPSPPICMMNALVRALTDSTP 411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 412 RDLDYSRYCPTDQAAAGTDAEH-----VQQFYNLLTASIDVSRSWAEKIPGFTDLPK 463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              581 SKVLGALVELRKICTLGLQRIFYLKLEDLVSPPSIIDKL 619
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507 AL----DILYPSHOLPEEFM 522
                                     600 RIFYLKLEDLVSPPSIIDKLFL 621
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Search completed: March 12, 2005, 17:52:00

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OM protein - protein search, using sw model

Run on:

March 12, 2005, 17:40:16; Search time 176 Seconds (without alignments) 1821.373 Million cell updates/sec

Title: Perfect score: Sequence:

US-10-608-863-2 3337 1 MPCVQAQYSPSPPGSSYAAQ......EDLVSPPSIIDKLFLDTLPF 626

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

Total number of hits satisfying chosen parameters: 1612378 segs, 512079187 residues Searched:

1612378

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	Q92570 homo sapien	097726 sus scrofa	P51179 rattus norv	Ogqzbe mus musculu	097727 sus scrofa	P43354 homo sapien	Q06219 mus musculu	7	-	Q6dh08 brachydanio		P51666 canis famil	Q8n3v2 homo sapien	homo	homo	Ofzmm6 homo sapien	Q6iny4 xenopus lae	Q04913 xenopus lae	Q7t0v3 xenopus lae	P22829 rattus norv	P12813 mus musculu		Q7q4c6 anopheles g	-		Q8inu7 drosophila	Q9rlw4 mus musculu	P49870 bombyx mori		P22448 gallus gall	Q9w6b3 coturnix co
COLUMNIC	QI	NR43_HUMAN	097726	NR43_RAT	NR43_MOUSE	097727	NR42 HUMAN	NR42_MOUSE	NR42_RAT	Q98TQ3	Фернов	06NXU0	NR41_CANFA	Q8N3 <u>V</u> 2	NR41_HUMAN	Q6IBU8	Q6 ZMM6	Q6INY4	NR42_XENLA	Q7T0V3	NR41_RAT	NR41_MOUSE	Q6GMG3	Q7Q4C6	Q9U4L1	HR38_DROME	QBINU7	Q9R1W4	HR38_BOMMO	NHR6_CAEEL	RRB CHICK	RRB_COTJA
	DB :	-	~	Н	Н	~	-	Н	Н	~	~	~	-1	~	Н	~	~	~	٦	~	н	Н	~	7	~	н	~	~	H	-	-	н
	Match Length DB	626	643	628	627	446	598	598	598	909	586	535	598	598	598	598	652	577	577	577	597	601	574	808	545	1073	556	392	360	619	455	455
ouerv	Match	99.9	93.9	92.1	91.5	62.9	52.5	52.3	52.0	50.3	47.6	47.1	41.1	41.0	41.0	40.9	40.5	40.5	40.5	40.5	39.6	39.5	37.6	36.5	35.9	35.7	35.0	31.7	30.7	16.6	16.3	16.3
	Score	3333	3133.5	3074	3054.5	2099.5	1751	1746	1736	1677	1588	1572	1371	1368	1367	1364	1353	1351.5	1350.5	1350.5	1322.5	1316.5	1254	1219.5	1197.5	1190.5	1168.5	1057.5	1023	554.5	545	545
Result	No.	1	7	m	4	ß	9	7	ω	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31

QGaw80 homo sapien P22605 mus musculu P28702 homo sapien P11416 mus susculu P97513 mus spretus P10826 homo sapien Q95153 mustela vis Q6pAh5 homo sapien Q61048 homo sapien Q61048 homo sapien Q61048 homo sapien P28704 mus musculu P18514 noccphtalm Q6mgb3 rattus norv	
QGAWBO RRB MOUSE RXRB HUWAN RRA MOUSE P97513 RRB HUWAN RRA HUWAN Q95153 Q6F2H5 Q6F2H5 Q6IN4B RRA CHICK RXRE MOUSE RRA NOTVI	
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ALIGNMENTS

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61 FVEGYSSNYELKPSCVYQMQRPLIKVEEGRAPSYHHHHHHHHHHHHHHHHQQQPQQPSIPPA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSPEDEVLPSTSMYFKQSPPSTPTTPAFPPQAGALWDEALPSAPGCIAPGPLLDPPMKAV 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSPEDEVLPSTSMYFKQSPPSTPTTPAFPPQAGALWDEALPSAPGCIAPGPLLDPPMKAV 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCPVDKRRRNRCQYCRFQKCLSVGMVKE 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCPVDKRRNRCQYCRFQKCLSVGMVKB 360
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                                                                                                                                                                                                                                                                                                                                         1 MPCVQAQYSPSPPGSSYAAQTYSSEYTTEIMNPDYTKLTMDLGSTEITATATTSLPSIST
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                                                                                                                                                                                                                                                                                          1 MPCVQAQYSPSPBGSSYAAQTYSSEXTTEIMNPDYTKLTMDLGSTEITATATTSLPSIST
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Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Badimon L.;
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                                                                                                                                                                       Length
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240 G -> S (in Ref. 3 and 4).
454 K -> R (in Ref. 1).
579 T -> N (in Ref. 1).
585 G -> V (in Ref. 1).
68199 MW, 40D18DA8FEF999IEC CRC64;
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Pred. No. 1.4e-168;
0; Mismatches 1;
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Best Local Similarity 99.8
Matches 625, Conservative
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                                                                                                                  626 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                Isold=092570-2; Sequence=VSP_003712, VSP_003713; TISSUE SPECIFICITY: High expression of isoform alpha in skeletal muscle. High expression of isoform beta in skeletal muscle and low expression in fetal brain and placenta.

DISEASE: Involved in Ewing's sarcoma through chromosomal translocations t(9;22) (q22-31;q11-12) which involve EWS and NR4A3. DISEASE: Involved in a form of extraskeletal myxoid chondrosarcomas (EWC) through a chromosomal translocation t(9;17) (q22;q11) that involves TAF2N and NR4A3. SIMILARITY: Belongs to the nuclear hormone receptor family. NR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YCPTDOAAAGTDABHVQQFYNLLTA -> VSFMISCFQMND QGLYLWLLVTRVD (in isoform Beta). Frid-VSP 003712. Missing (in isoform Beta). /Frid-VSP_003713.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subfamily.
-!- CAUTION: Ref.2 sequence differs from that shown due to frameshifts
in positions 4 and 20.
                    MEDLINE=98241504; PubMed=9573341, DOI=10.1016/80378-1119(98)00095-X; Ohkura N., Ito M., Tsukada T., Sasaxi K., Yamsguchi K., Miki K.; "Alternative splicing generates isoforms of human neuron-derived orphan receptor-1 (NOR-1) mRNA."; Gene 211.79-85(1998).
-!- FUNCTION: Binds to the BlA response-element.
-!- SUBCELJULAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0398; STRDIDENMONER.
PRINTS; PRO0398; STRDIDENMER.
PROSON PRO0047; STRDIDENMER.
PROSTITS; PRO0047; STRDIDENMER.
PROSTITS; PRO0047; STRDIDENMER.
Alternative splicing; Chromosomal translocation; DNA-binding;
Nuclear protein; Proto-oncogene; Receptor; Transcription regulation;
DNA_BIND 292 357 Nuclear receptor-type.
ZN FING 292 312 C4-type.
ZN FING 328 352 C4-type.
ZN FING 328 352 C4-type.
DOMAIN 440 490 Ligand-binding (Potential).
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GO; GO:0005488; F:binding; TAS.
GO; GO:0003707; F:steroid hormone receptor activity; TAS.
GO; GO:0004887; F:thyroid hormone receptor activity; TAS.
InterPro; IPR00536; Hrmon recept 119.
InterPro; IPR00536; Hrmon receptor.
InterPro; IPR008946; Str ncl receptor.
InterPro; IPR001628; Znf C4steroid.
Pfam; PF00104; Hormone recep; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C4-type.
C4-type.
Ligand-binding (Potential).
Poly-His.
                                                                                                                                                                                                                                                         Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                 IsoId=Q92570-1; Sequence=Displayed;
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EMBL; S81243; AAB36006.1; ALT_INIT.
EMBL; X89894; CAA61994.1; --
EMBL; D85241; BAA28608.1; --
EMBL; D85242; BAA31221.1; --
HSSP; P43354; IOVL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D78579; BAA11419.1; -.
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TRANSFAC; T04753; -.
Genew; HGNC:7982; NR4A3.
  TISSUE=Skeletal muscle;
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443
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InterPro; IPR000536; Hrmon_recept_lig.
InterPro; IPR001723; Stdhrmn_receptor.
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                                                                                NR43 RAT (
P51179; Q63516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       subfamily.
                                                                NR43 RAT
                                                                                 3,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                --QHQQPSIPPASSPEDEVLPSTSMYFKQSPPSTPTTPAFPPQAGALWDEALPSAPGCIA 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGPLLDPPMKAVPTVAGARFPLFHFKPSPPHPPAPSPAGGHHLGYDPTAAAALSLPLG-- 226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSSSGEGTCAVCGDNAACQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCPVDKRRRNR 343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---AAAAAGSQAAALESHPYGLPLAKRAAPLAFPPLGLTPSPTASSLLGESPSLPSPPSR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MPCVQAQYSPSPPGSSYAAQTYSSEYTTEIMNPDYTKLTMDLGSTEITATATTSLPSIST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MPCVQAQYSPSPPGSSYAAQTYGSEYTTEIMNPDYTKLTMDLGSTEITATATTSLPSFST
                                                                                                                                                                                                                                                                                                                                         PROMITY PS00031; NUCLEAR RECEPTOR, 1.

DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
Transcription regulation; Zinc; Zinc-finger.

SEQUENCE 643 AA; 70077 MW; 20596A4222FB4CA7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
-i- SIMILARITY: Belongs to the nuclear hormone receptor family.
EMBL; AJ011767; CAA09763.1; -.
HSSP; P43354; 10VL.
                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 643;
                                            GO: GO:0005634; C:nucleus; IEA.
GO: GO:0003707; F:steroid hormone receptor activity; IEA.
GO: GO:0003700; F:transcription factor activity; IEA.
GO: GO:0006355; P:regulation of transcription, DNA-dependent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         22; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                         Match 93.9%; Score 3133.5; DB Local Similarity 92.4%; Pred. No. 5e-158; es 594; Conservative 10; Mismatches 23
                                                                                                        InterPro; IPR000336; Hrmon recept 119.
InterPro; IPR003072; NOR1 receptor:
InterPro; IPR003070; Nucorph. receptor:
InterPro; IPR003070; Str. ncl. receptor:
InterPro; IPR008946; Str. ncl. receptor:
InterPro; IPR001628; Str. ncl. receptor:
Pfam; PF00104; Hormone recep; 1.
Pfam; PF00105; zf. c4; I.
                                                                                                                                                                                                                                  PRINTS; PRO1286; NORNUCRECPTR.
PRINTS; PRO1284; NUCLEARECPTR.
PRINTS; PRO0398; STRDHORNONER.
PRINTS; PRO0047; STROIDFINGER.
PRINTS; PRO0047; ZIE_C48teroid; 1.
SMART; SM00430; HOLI; 1.
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Isodd=P51179-1; Sequence=Displayed;
Name=2; Synonyms=NOR-2;
IsoId=P51179-2; Sequence=VSP_010085, VSP_010086;
-1-TISSUG SPRECIFICITY: Expressed at high levels in cultured apoptotic neuronal cells and fetal brain, and at low level in adult brain.
-1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N.A. (ISOFORM 2).
SEQUENCE FROM N.A. (ISOFORM 2).
STRAIN-Sprague-Dawley; TISSUE=Brain;
MEDLINE=96000221; PubMed-0756683; DOI=10.1016/0014-5793(95)00998-O;
Petropoulos I., Part D., Orboa A., Zakin M.M., Lamas E.;
"NOR-2 (neuron-derived orphan receptor), a brain zinc finger protein, is highly induced during liver regeneration.";
FEBS Lett. 372:273-278(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Name=Nr4a3; Synonyms=Norl;
Rattuu norvegicus (Rat).
Eukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pena de Ortiz S., Cannon M.M., Jamieson G.A. Jr.;
"Expression of nuclear hormone receptors within the rat hippocampus:
identification of novel orphan receptors";
Brain Res. Mol. Brain Res. 23:278-283(1994).
-!- FUNCTION: Binds to the B1A response-element.
-!- SUBCELULAR LOCATION: Nuclear (Potential).
                                                                                                                                                                                                                                                                                                                                                                                   receptor NOR-1/NOR-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
STRAIN=Wistar; TISSUE=Brain;
MEDLINE=95110148; PubMed=7811288;
Ohkura N., Hijikuro M., Yamanoto A., Miki K.;
"Molecular cloning of a novel thyroid/steroid receptor superfamily gene from cultured rat neuronal cells.";
Biochem. Biophys. Res. Commun. 205:1959-1965(1994).
601 LRALVELRKICTLGLQRIFYLKLEDLVSPPSIIDKLFLDTLPF 643
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                                                                                                                                                                                                                                                           01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Orphan nuclear receptor NR4A3 (Nuclear hormone
                                                                                                                                                                                           Ź
                                                                                                                                                                                           628
                                                                                                                                                                                                                                                                                                                                                                                                                       (Neuron-derived orphan receptor 1/2)
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SEQUENCE OF 318-345 FROM N.A.
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TRANSFAC; T02768; -.
TRANSFAC; T04752; -.
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PubMed=7914660;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            298 GDNAACQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCPVDKRRRNRCQYCRFQKCLSV 357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDNAACQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCPVDKRRRNRCQYCRFQKCLSV
                                                                                                                                                                    YCPIDQATAG -> VSSVNRFEWF (in isoform 2).
(FITId=VSP 010085.
Missing (In isoform 2).
/FITId=VSP_010086.
/FITId=VSP_010086.
P -> Q (in Ref. 2).
P -> Q (in Ref. 2).
9AC285D9A65226D9 CRC64;
                                                                                                                                                                                                                                                              Gaps
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                                 PRINTS; PRO0398; STRDHORMONER.
PRINTS; PRO0047; STRCHOFINGER.
PRODOM; DALF ZAF C4steroid; 1.
SWART; SW00430; HOLI; 1.
SWART; SW00399; ZAF C4; 1.
PROSITE; PS00031; NUCLEAR EECEPTOR; 1.
ALLETHALIVE SPLICING; DNA-bInding; Nuclear protein; Receptor;
Transcription regulation; Zinc-finger.
                                                                                                                                                                                                                                            Length 628;
                                                                                                                 C4-type.
C4-type.
Ligand-binding (Potential).
Poly-His.
Poly-Cln.
                                                                                                                                                                                                                                                           Indels
                                                                                                         Nuclear receptor-type
                                                                                                                                                                                                                                          92.1%; Score 3074; DB 1; 1
92.2%; Pred. No. 6.9e-155;
ive 12; Mismatches 29;
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InterPro, IPR008946; Str.ncl.receptor.
InterPro; IPR001628; Znf_C4steroid.
Pfam; PF00104; Hormone.recep; 1.
Pfam; PF00105; zf-C4; 1.
                                                                                                                                                                                                                  18 P
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Matches 582; Conservative 1
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354
492
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628 AA;
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       brain.
SIMILARITY: Belongs to the nuclear hormone receptor family, NR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Cell Biol. 19:121-130 (2000).
--- SUBCELLULAR LOCATION: Nuclear (Potential).
--- SUBCELLULAR LOCATION: Nuclear (Potential).
--- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
Name=1; Synonyms=Long;
Isola-090ZB6-1; Sequence=Displayed;
Name=2; Synonyms=Short, TECdeltaC;
Name=2; Synonyms=Short, TECdeltaC;
Isola-090ZB6-2; Sequence=VSP 010083; VSP 010084;
--- TISSUE SPECIFICITY: Ubiquitous. Highest levels of expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORMS 1 AND 2). WBDLLNB=20163713; Pubmed=10701778; DOI=10.1089/104454900314636; Maltais A., Labelle Y. ^{\prime} "Structure and expression of the mouse gene encoding the orphan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART, SM00399, ZNF C4, 1.
PROSITE, PS00031, NUCLEAR RECEPTOR, 1.
Alternative splicing, DNA-binding, Nuclear protein, Receptor,
Transcription regulation, Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                          receptor TEC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C4-type.
Ligand-binding (Potential).
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                                                                                                                                                                                 NR43_MOUSE STANDARD; PRT; 627 AA. 090ZB5; 05-UUL-2004 (Rel. 44, Created) 55-UUL-2004 (Rel. 44, Last sequence update) 05-UUL-2004 (Rel. 44, Last annotation update) 05-UUL-2004 (Rel. 44, Last annotation update) 05-UUL-2004 (Rel. 44, Last annotation update) Orphan nuclear receptor NR4A3 (Orphan nuclear I (Translocated in extraskeletal chondrosarcoma). Mus musculus (Mouse).
598 QGLQRIFYLKLEDLVSPPSVIDKLFLDTLPF 628
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EMBL; AF191212; AAF05623.1; -...
MSSP; P43344; 10VU.
MGD; MGI:1352457; Nr4a3.
InterPro; IPR001073; Schhrun recept_lig.
InterPro; IPR001723; Schhrun receptor.
InterPro; IPR001946; Str ncl receptor.
InterPro; IPR001946; Str ncl receptor.
InterPro; IPR00189; Str ncl receptor.
Pfam; PF00104; Hormone recep; 1...
PRINTS; PR00198; STRONDFNNONER.
PRINTS; PR00047; STRONDFNNORE.
PRINTS; RR00439; STRONDFNNORE.
SMART; SM00430; ADF.C4; 1...
SMART; SM00430; ADF.C4; 1...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Poly-His.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nuclear receptor TEC.";
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GO; GO:0005634; C:nucleus; IEA.

GO; GO:0004879; F:ligand-dependent nuclear receptor activity; IEA.

GO; GO:0004879; F:ligand-dependent nuclear receptor activity; IEA.

RO; GO:0003700; F:ransacription factor activity; IEA.

RO; GO:000535; F:regulation of transcription, DNA-dependent; IEA.

InterPro; IFR003072; NORI_receptor.

R InterPro; IFR003072; NUCCPTh_receptor.

R InterPro; IFR001286; NUCLEARECPTR.

PRINTS; PR001286; NORNUCRECPTR.

PRINTS; PR00047; STR01DFINGER.

R PRINTS; PR00047; STR01DFINGER.

R PRODOM; PD000035; Znf_C4teroid; 1.

RNART; SM00399; Znf_C4teroid; 1.

RNART; R00031; NUCLEAR RECEPTOR; 1.

RNART; R00031; NUCLEAR RCEFTOR; 1.

RNART; R00031; NUCLEAR RCEFTOR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 AAAAAAAGSQAAALEGHPYGLPLAKRAAALAFSPLGLTTSPTTSSLLGESPSLPSPNR 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PGPLLDPPMKAVPTVAGARFPLFHFKPSPPHPPAPSPAGGHHLGYDPTAAAALSLPLG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CQYCRFQKCLSVGMVKEVVRTDSLKGRRGRLPSKPKSPLQQEPSQPSPPSPPVCMMALV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FVEGYSSNYELKPSCVYQMQ----RPLIKVEEGRAPSYHHHHHHHHHHHHHHQQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -- QHQQPSIPPASSPEDEVLPSTSMYFKQSPPSTPTTPAFPPQAGALWDEALPSAPGCIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSSSGEGTCAVCGDNAACQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCPVDKRRRNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MPCVQAQYSPSPPGSSYAAQTYGSEYTTEIMNPDYTKLTMDLGSTEITATATTSLPSFST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---AAAAAGSQAAALESHPYGLPLAKRAAPLAFPPLGLTPSPTASSLLGESPSLPSPPSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CQYCRFQKCLSVGMVKEVVRTDSLKGRRGRLPSKPKSPLQQEPSQPSPPSPPICMMNALV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MPCVQAQYSPSPPGSSYAAQTYSSEYTTEIMNPDYTKLTMDLGSTEITATATTSLPSIST
                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 446;
                                                                                                                                                                                                                                                                                                                                                                                                                                              18; Indels
                                                                                                                                                                                                                                                                                                                                                                                            62.9%; Score 2022...,
89.9%; Pred. No. 1.8e-103;
rive 9; Mismatches 18;
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Last annotation update)
or NR4A2 (Orphan nuclear
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01-NOV-1995 (Rel. 32, Created)
NOV-1995 (Rel. 32, Last seq
25-OCT-2004 (Rel. 45, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 391; Conservative
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SEQUENCE FROM N.A.
TISSUE=Blood;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           477 ELFVLRLSIRSNTAEDKFVFCNGLVLHRLQCLRGFGEWLDSIKDFSLNLQSLNLDIQALA 536
                                                                                                                                                                                                                                                                                                                                    117 IPPASSPEDEVLPSTSMYFKQSPPSTPTTPAFPPQAGALWDEALPSAPGCIAPGPLLDPP 176
                                                                                                                                                                                                                                                                                                                                                             AALESHPYGLPLAKRAAPLAFPPLGLTPSPTASSLLGESPSLPSPPSRSSSGGGTCAVC 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AALEGHPYGLPLAKRTATLTFPPLGLTASPTASSLLGESPSLPSPPNRSSSSGEGTCAVC 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GDNAACQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCPVDKRRRNRCQYCRFQKCLSV 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GWVKEVVRTDSLKGRRGRLPSKPKSPLQQEPSQPSPPSPPICMMNALVRALTDATPRDLD 416
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                                                                                                                                                                                FVEGYSSNYELKPSCVYOM----ORPLIKVEEGRAPSYHHHHHHHHHHHHOOOHQOPS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GDNAACQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCPVDKRRNRCQYCRFQKCLSV
                                                                                                                                                            1 MPCVQAQYSPSPPGSSYAAQTYSSEYTTEIMNPDYTKLTMDLGSTEITATATTSLPSIST
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                                                                                                                 Gaps
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Sus.
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                                                                      DB 1; Length 627;
                                                                                                                 Indels
      /FIId=VSP 010084.
2F49CB4CBDE315A8 CRC64;
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-UNA-2003 (TrEMBLrel. 24, Last annotation update)
Neuron-derived orphan receptor-1 beta.
                                                                    Ouery Match 91.5%; Score 3054.5; DB 1; Best Local Similarity 91.8%; Pred. No. 7.4e-154; Matches 579; Conservative 12; Mismatches 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            596 LGLORIFYLKLEDLVSPPSIIDKLFLDTLPF 626
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                             68454 MW;
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                             SEQUENCE
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110

9

Gaps

17;

180

283

343

403 420

uclear receptor NURR1) (Transcriptionally inducible Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. φ

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Attaubberg R.L., Feingold E.A., Grouse L.H., Derged G.G.,
Riausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bahat N.K.,
A plokins R.F., Jordan H., Moore T., Mang J., Hsieh F.,
Bill Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toophyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunzarene P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gaby L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakealey R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Warra M.A.,
Butterfield Y.S.N., Warra M.A.,
Butterfield W.S., Oones S.J.M., Marra M.A.,
                                                                                                                                    TISSUE=Fibroblast;
MEDIATE-9931404; PubMed=10216262; DOI=10.1016/S0378-1119(99)00065-7;
IChinose H., Obye T., Suzuki T., Sumi-Ichinose C., Nomura T.,
Hagino Y., Nagatsu T.;
"Molacular cloning of the human Nurr1 gene: characterization of the human gene and cDNAs.";
Gene 230:233-239(1999).
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-99234103; PubMed=10216261; DOI=10.1016/S0378-1119(99)00064-5;
TOril T., Kawarai T., Nakamura S., Kawakami H.;
"Organization of the human orphan nuclear receptor Nurrl gene.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=95183071; PubMed=7877627; DOI=10.1210/me.8.11.1583; Mages H.W., Rilke O., Bravo R., Senger G., Kroczek R.A.; "NOT, a buman immediate-early response gene closely related steroid/thyroid hormone receptor NAKI/TR3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                             Mol. Endocrinol. 8:1583-1591 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequences."
                                                                                                                                                                                                                                                                                                                                                                         Gene 230:225-232(1999)
                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and mouse cDNA
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SIMILARITY: Belongs to the nuclear hormone receptor family. NR4

subfamily.

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EMBL; X75918; CAA53518.1; -.

SISTFVEGYSSNYELKPSCVYQM----QRPLIKVEEGRAPSYHHHHHHHHHHHHHQQQH 112 113 QOPSIPPASSPEDEVLP-STSMYFKQSPPSTPTTPAFPPQAGALWDEALPSAPGCIAPGP 171 LLDPPMKAVPT-----VAGARFPLFHFKPSPPHPPA-------PSPAG 207 149 LHNFHQNYVATTHMIEQRKTPVSRLSLFSFKQSPPGTPVSSCQMRFDGPLHVPMNPEPAG 208 208 GHHLGYDPTAAAALSLPLGAAAAAGSQAAALESHPYGLP-LAKRAAPLAFPPLGLTPSPT 266 ASQLL--DTQVPSPPSRGSPSNEGLCAVCGDNAACQHYGVRTCEGCKGFFKRTVQKNAKY 297 VCLANKNCPVDKRRRNRCQYCRFQKCLSVGMVKEVVRTDSLKGRRGRLPSKPKSPLQQEP 386 387 SQPSPPSPPICMMNALVRALTDSTP--RDLDYSRY-CPTDQAAAGTDAEHVQQFYNLLTA 443 353 QEPSPPSPPVSLISALVRAHVDSNPAMTSLDYSRFQANPDYQMSGDDTQHIQQFYDLLIG 412 1 MPCVQAQYSPSPPGSSYAAQTY----SSEYTTEIMNPDYTKLTMDLGSTEITATATTSLP ASSLLGESPSLPSPPSRSSSSGEGTCAVCGDNAACQHYGVRTCEGCKGFFKRTVQKNAKY 74; Mismatches 121; Indels 108; Gaps SFSTFMDNYSTGYDVKPPCLYQMPLSGQQSSIKVEDIQMANYQQHSH-Length Nuclear receptor-type. Score 1751; DB 1; Pred. No. 6.7e-85; regulation; Zinc-finger. Pro-rich. PDB; 10VL; X-ray; A/B/C/D/E/F=328-598. TRANSFAC; T02742; -. AB017586; BAA75666.1; -. AB019433; BAA77328.1; -. BC009288; AAH09288.1; -. S77154; AAB33999.1; -. 52.5%; Matches 363; Conservative Genew; HGNC:7981; NR4A2. H-InvDB; HIX0002518; MIM; 601828; -. PIR; A57040; A57040 598 AA; Similarity Transcription DNA_BIND ZN_FING ZN_FING DOMAIN DOMAIN 240 57 59 106 172 267 298 327 SEQUENCE Query Match Local DOMAIN DOMAIN δ g ઠે a ò 유 ð 셤 ò g à 셤 à 셤 à g

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                                    472
                                                                                                                                          592
                                                               LOCLRGFGEWLDSIKDFSLNLQSLNLDIQALACLSALSMITERHGLKEPKRVEELCNKIT 563
                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUB=Brain;
MEDLINE=9114912; PubMed=1491694; DOI=10.1210/me.6.12.2129;
Law S.W.; Conneely O.M., Demayo F.J., O'Malley B.W.;
Iaw G.W.; Identification of a new brain-specific transcription factor, NURRI.";
Mol. Endocrinol. 6:2129-2135(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FUNCTION: Probable nuclear receptor that regulates gene expression in brain tissue.
                                                                             SIDVSRSWAEKI PGFTDL PKEDQTLLI ESAFLELFVLRLSIRSNTAEDKFVFCNGLVLHR
                                                                                                                  SSLKDHQ--SKGQALEPTE-SKVLGALVELRKICTLGLQRIFYLKLEDLVSPPSIIDKLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neonates and decreases in the adult. SIMILARITY: Belongs to the nuclear hormone receptor family. NR4
                                                                                                                                                                                                                                                           NR42 MOUSE STANDARD; PRT; 598 AA.

Q06219; O08690;

Q1-JUN-1994 (Rel. 29, Last sequence update)

O1-JUN-1994 (Rel. 29, Last annotation update)

O5-JUN-2004 (Rel. 44, Last annotation update)

Orphan nuclear receptor NR4A2 (Orphan nuclear receptor NURR1) (NURrelated factor 1).
                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=129/SvJ;
MEDLINE=97288523; PubMed=9143501; DOI=10.1006/geno.1997.4677;
MEDLINE=97288523; PubMed=9143501; Noi=10.1006/geno.1997.4677;
MEDLINE=97288523; PubMed=9143501; Noi=10.1006/geno.1997.4677;
"Organization, Asquence, chromosomal localization, and promoter identification of the mouse orphan nuclear receptor Nurrl gene.";
Genomics 41:250-257(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in the embryo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [BoId=006219-2; Sequence=VSP_003710, VSP_003711;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: Brain.
DEVELOPMENTAL STAGE: Expression begins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q06219-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLULAR LOCATION: Nuclear.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; S53744; AAB25138.1; -.
EMBL; U86783; AAC53153.1; -.
EMBL; U86783; AAC53154.1; -.
                                                                                                                                                                                                                                                                                                                                                      Name=Nr4a2; Synonyms=Nurr1;
                                                                                                                                                                     LDTLPF 626
                                                                                                                                                                                              LDTLPF 598
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=NURR1A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=NURR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIDVSRSWAEKIPGFTDLPKEDQTLLIESAFLELFVLRLSIRSNTAEDKFVFCNGLVLHR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 LHNFHQNYVATTHMIEQRKTPVSRLSLFSFKQSPPGTPVSSCQMRFDGPLHVPMNPEPAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GHHLGYDPTAAAALSLPLGAAAAAGSQAAALESHPYGLP-LAKRAAPLAFPPLGLTPSPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.3%; Score 1746; DB 1; Length 598;
54.4%; Pred. No. 1.2e-84;
ive 75; Mismatches 121; Indels 108;
                                                                                                                                                                                                                                                                                                            SMART; SM00399; ZNF C4; 1.
PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
Alternative splicing; DNA-binding; Nuclear protein; Receptor;
Transcription regulation; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             106 ----EPPQS---EEMMPHSGSVYYKPSSPPTPSTPSFQVQHSPMMDD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Missing (In isoform NURRIA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pro-rich.
Ligand-binding (Potential)
S -> I (in isoform NURRIA)
/FrId=VSP 003710... NURBIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66592 MW; DIACSEBZFFBBD366 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Nuclear receptor-type.
C4-type.
C4-type.
                                    GO; GO:005634; C:nucleus; IDA.
GO; GO:0005634; C:nucleus; IDA.
GO; GO:0007399; P:neurogenesis; IMP.
GO; GO:0007399; P:neurogenesis; IMP.
GO; GO:0042053; P:neurogenesis; IMP.
GO; GO:0042053; P:neurogenesis; IMP.
GO; GO:0042053; P:neurogenesis; IMP.
InterPro; IPR001723; Stdhrmn receptor.
InterPro; IPR001628; Str_ncl_receptor.
InterPro; IPR001628; Str_ncl_receptor.
InterPro; IPR001628; Str_ncl_receptor.
Pfam; PF00104; Hormone recep; I.
PRINTS; PR00047; STROHORNONER.
PRINTS; PR00047; STROHORNONER.
PROMOM; PR000039; STR_C4steroid; I.
SWART; SM00430; HOLI; I.
                                                                                                                                                                                                                                                                                                                                                                                                                     Pro-rich.
                                                                                                                                                                                                                                                                                                                                                                                                Gln-rich.
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TRANSFAC; T04312; -. MGD; MGI:1352456; Nr4a2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      456
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DOMAIN 8
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DNA BIND
ZN FING
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ZN FING
DOMAIN
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or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    113 QOPSIPPASSPEDEVLP-STSMYFKQSPPSTPTTPAFPPQAGALWDEALPSAPGCIAPGP 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLDPPMKAVPT-----VAGARFPLFHFKPSPPHPPA--------PSPAG 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LHNFHQNYVATTHMIEQRKTPVSRLSLFSFRQSRPGTPVSSCQMRFDGPLHVPMNPEPAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ASSLLGESPSLPSPPSRSSSSGEGTCAVCGDNAACQHYGVRTCEGCKGFFKRTVQKNAKY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQPSPPSPPICMMNALVRALTDSTP--RDLDYSRY-CPTDQAAAGTDAEHVQQFYNLLTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MPCVQAQYSPSPPGSSYAAQTY----SSEYTTEIMNPDYTKLTMDLGSTEITATATTSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ASOLL -- DIQVPSPPSRGSPSNEGLCAVCGDNAACQHYGVRICEGCKGFFKRIVQKNAKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VCLANKNCPVDKRRRNRCQYCRPQKCLSVGMVKEVVRTDSLKGRRGRLPSKPKSPLQQEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
DNA-binding; Nuclear protein; Receptor; Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 1736; DB 1; Length 598;
; Pred. No. 4.2e-84;
74; Mismatches 123; Indels 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R -> A (in Ref. 2).
R -> P (in Ref. 3).
S -> P (in Ref. 2).
P -> A (in Ref. 1).
V -> G (in Ref. 2).
LISALVRA -> DGCPRQT (in Ref. 2).
D -> S (in Ref. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OAS4ED59FB70DEA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Nuclear receptor-type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                C4-type.
Pro-rich.
Liganch binding (
R -> A (in Ref.
R -> P (in Ref.
S -> P (in Ref.
P -> A (in Ref.
V -> G (in Ref.
                                                                                                          HSSP; P43354; 100L.
TRANSFAC; T04743; -.
TRANSFAC; T04743; -.
TRANSFAC; T04743; -.
INTERPRO; IPR000536; Hrmon recept_lig.
INTERPRO; IPR001723; Stdhrmn receptor.
INTERPRO; IPR001828; Stdhrmn receptor.
INTERPRO; IPR001828; Zhf_C4fleroid.
Pfam; PF00104; Hormone_receptor.
Pfam; PF00104; Hormone_recept; 1.
PRINTS; PR00195; STREADRANDER.
PRINTS; PR00047; STROIDFINGER.
PRODOM; PR000039; ZAFC4; 1.
SWART; SM00339; ADF_C4; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                     Pro-rich.
                                                                                                                                                                                                                                                                                                                                                                                                     Gln-rich
                                                EMBL; U01146; AAC52143.1; -. EMBL; L08859; AAA42058.1; -. EMBL; U7245; AAC53115.1; -. PIR; I84692; I84692.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66621 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 54.2°
Matches 361; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   138
2333
3328
3328
3323
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I differentially induced in the hippocampal dentate gyrus by electromically verselves. Windled selfaures.

Brain Res. Mol. Brain Res. 47:251-261(1997).

-1- FUNCTION: Probable nuclear receptor. May confer liver-specific regeneration along with HRR.

-1- FUNCTION: Probable nuclear receptor. May confer liver-specific regeneration along with HRR.

-1- SUBCELLULAR LOCATION: Nuclear in quiescent liver but is rapidly induced following partial hepatectomy and is specific to hepatic growth as it is not induced in other mitogen-treated cells. Expressed at very low levels in the lung, spleen and cells. Expressed at very low levels in the lung, spleen and cells. Signal in the brain.

-1- SIMILARITY: Belongs to the nuclear hormone receptor family. NR4
                                                                                                                                                                                                                                                           NW42 RAT
O07917; 035865;
01-0CT-1994 (Rel. 30, Created)
15-JUL-1999 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Orphan nuclear receptor NR4A2 (Orphan nuclear receptor NURR1) (NUR-
1312) (Nuclear orphan receptor HZF-3).
Nume-NY421; Synonyma-HZF-3, Nurr1, Rnr1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ŏ
                             LQCLRGFGEWLDSIKDFSLNLQSLNLDIQALACLSALSMITERHGLKEPKRVEELCNKIT
                                                                             564 SSLKDHQ--SKGQALEPTE-SKVLGALVELRKICTLGLQRIFYLKLEDLVSPPSIIDKLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scearce L.M., Laz T.M., Hazel T.G., Lau L.F., Taub R.;
"RNR-1, a nuclear receptor in the NGFI-B/Nur77 family that is rapidly induced in recentaing liver.";
J. Biol. Chem. 268:8855-8861(1993).
                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRANDARY; TISSUE-Brain; STRANDARY; PubMed=9221923; DOI=10.1016/S0169-328X(97)00056-9; Xing G.Q., Zhang L.X., Zhang L., Heynen T., Li X.L., Smith M.A., Weiss S.R.B., Feldman A.N., Detera-Wadleigh S., Chuang D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Sprague-Dawley, TISSUE=Hippocampus,
MEDLINE=94335560; PubMed=7914660; DOI=10.1016/0169-328X(94)90235-6;
de Ortiz S., Cannon M.M., Jamieson G.A.;
"Expression of nuclear hormone receptors within the rat hippocampus:
identification of novel orphan receptors.";
Brain Res. Mol. Brain Res. 23:278-283(1994).
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                                                                                                                                               626
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TISSUE=Liver;
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SISTFVEGYSSNYELKPSCVYQM----QRPLIKVEEGRAPSYHHHHHHHHHHHHHQQQH 112
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                                                                                                                                                                                                                                                        249 QVPSPPSRGSPSNEGLCAVCGDNAACQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCP
                                                                                                                                                                                                                                                                                                        396 ICMMNALVRALTDSTP--RDLDYSRY-CPTDQAAAGTDAEHVQQFYNLLTASIDVSRSWA
                                                                                                                                                                                                                                                                                                                                                             QQPSIPPASSPEDEVLPSTSMYFKQSPPSTPTTPAFPPQAGALWDEALPSAPGCI-----
                                                                                                         102 ÓSHLÞÞQS--EEMIAHTGPMYFKPSSÞHAÞSTÞNFQVQPNHMWED-----ÞGSLHSFHQ
                                                                                                                                   ----APGPLLDPPMKAVPTVAGARFPLFHFKPSPPHPPAPSPAGGHHLGYDPTAAAALSL
                                                                                                                                                           155 NYVAATSHMMB--QRKTPV---SRLSLFSFKQSPPGTPVSS----CQMRFDG-----
                                                                                                                                                                                                            198 PLHVSMTHDNPGAHRGLDGQSFAVPSAIRKQAGLAFP-----HSLQLSHGHQLVDS
                                                                                                                                                                                                                                                                                           VDKRRRINRCQYCRPQKCLSVGMVKEVVRTDSLKGRRGRLPSKPKSPLQQBPSQPSPPSPP
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    MPCVQAQYGSSPQGASPASQSYSYHTAGEYSCDFLTPEFVKFSMDLTNTEI - -TATTSLP
                                                                                                                                                                                     PLGAAAAAGSQAA--ALESHPYGLPLA-KRAAPLAFPPLGLTPSPTASSLLGESPSL---
                                                                                                                                                                                                                                         --PSPPSRSSSSGEGTCAVCGDNAACQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       544 NSGGLNRPNYLSKLLGKLPELRTLCTQGLQRIFYLKLEDLVPPPAIIDKLFLDTLPF
                                           25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28, 25-OCT-2004 (TrEMBLrel. 28,
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                                                                                           LOCLRGFGEWLDSIKDFSLNLQSLNLDIQALACLSALSMITERHGLKEPKRVEELCNKIT
                                       SIDVSRSWAEKIPGFTDLPKEDQTLLIESAFLELFVLRLSIRSNTAEDKFVFCNGLVLHR
                                                         SSLKDHQ--SKGQALEPTE-SKVLGALVELRKICTLGLQRIFYLKLEDLVSPPSIIDKLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00031, NUCLEAR RECEPTOR; 1.
DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
Transcription regulation; Zinc, Zinc-finger.
SEQUENCE 600 AA; 66925 MW; BBSFEL6987DBFBAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Actinopterygii, Neoperygii, Teleostei, Buteleostei, Neoteleostei, Acanthomorpha, Acanthopterygii, Percomorpha, Atherinomorpha, Beloniformes, Adrianichthyidae, Oryziinae, Oryzias.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.3%; Score 1677; DB 2; Length 600; 53.7%; Pred. No. 5.5e-81; ive 81; Mismatches 135; Indels 8
                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                    Oryzias latipes (Medaka fish) (Japanese ricefish).
                                                                                                                                                                                                                                                                                           600 AA
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InterPro; IPR003070; Nucorph receptor.
InterPro; IPR003073; NURR_receptor.
InterPro; IPR001723; Stdhrmn receptor.
InterPro; IPR008946; Str_ncl_receptor.
InterPro; IPR00858; Str_ncl_receptor.
Pfam; PF00104; Hormone recep; 1.
                                                                                                                                                                                                                                                                                                                     Created)
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PRINTS; PR01287; NURNUCRCPTR.
PRINTS; PR00198; STRDHORMONER.
PRINTS; PR00047; STRDIDFINGER.
PRODOM; PD000035; Znf_C48teroid; 1.
                                                                                                                                                                                                                                                                                           PRT;
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1-JUN-2001 (TrEMBLrel. 17,
1-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                          Nuclear receptor related 1.
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Best Local Similarity 53.7
Matches 353; Conservative
                                                                                                                                                                                                                                                                                           PRELIMINARY;
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SMART; SM00399; ZnF C
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MEDLINE-275, PubMed=12477932; DOI=10.1073/pnas.242603899; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausmar R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunararne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gibbs R.A., Villalon D.K., Muzly D.M., Sodergren E.J., Lu X., Gibbs R.A., Villalon D.K., Muzly D.M., Madan A., Rodrigues S., Sanchez A.,
                                                                                                                                         Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                            Last sequence update)
Last annotation update)
  586
                                        Created)
PRT;
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MPCVQAQXSBSPBGSSYAAQTYS----SEYTTEIMNPDYTKLTMDLGSTEITATATTSLP

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A MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Rad Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RAD Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.;
A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.;
A Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.;
A Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
Batchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
R. Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
R. Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
R. Helton E., Ketreman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Mhiting M. J., Skalska U., Schmutz J., Myers R.M., Butterfield Y.S.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
A Dones S.J., Marra M.A.;
T. "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                          485 SSNLQSMSLDVSAFSCIAALTIVTERHGLKEPKKAEELQNKLINCLKDQVSCSGEL----
                                                                                                                                                                                                                                                                                                                 521 SLNLQSLNLDIQALACLSALSMITERHGLKEPKRVEELCNKITSSLKDHQSKGQALEPTE
                                                                                                                                             LPKEDQTLLIESAFLELFVLRLSIRSNTAEDKFVFCNGLVLHRLQCLRGFGEWLDSIKDF
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GO; GO:0003707; F:steroid hormone receptor activity; IEA.
GO; GO:0003700; F:transcription factor activity; IEA.
GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
-! SUBCELLULAR LOCATION: Nuclear (By similarity).
-! SUBCELLULAR belongs to the nuclear hormone receptor family.
EMBL; BCO66899; AAH66890.1; -.
HSSP; P20393; 1A6Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              626
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05-UUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Nuclear receptor subfamily 4, group A, member 2, isoform d.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              581 SKVLGALVELRKICTLGLQRIFYLKLEDLVSPPSIIDKLFLDTLPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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InterPro; IPR003070; Nucorph_receptor.
InterPro; IPR003073; NURR_receptor.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR008946; Str ncl_receptor.
InterPro; IPR001628; Znf_C4sTeroid.
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Pfam; PF00104; Hormone_recep; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SISTFVEGYSSNYELKPSCVYQM----QRPLIKVEEGRAPSYHHHHHHHHHHHHHQQQH 112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PGPLLDPPMKAVPTVAGARFPLFHFKPSPPHPPAPSPA----GGHHLGYDPTAAALSLP 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 IGAAAAAGSQAAALESHPYGLPLAKRAAPLAFPPLGLTPSPTASSLLGESPSLPSPSRS 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              404 RALIDSTP--RDLDYSRYCPIDQAAAGIDAE-HVQQFYNLLIASIDVSRSWAEKIPGFID 460
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Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse CDNA sequences.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C -1- SUBCELLULAR LOCATION: Wiclear (By similarity).

-1- SUBLELLULAR LOCATION: Wiclear (By similarity).

-1- SUBLELLULAR LOCATION: Wiclear hormone receptor family.

EMBL BC076176; AAH76176.1; -.

R GO; GO:0003707; F:steroid hormone receptor activity; IEA.

GO; GO:0003707; F:steroid hormone receptor activity; IEA.

R GO; GO:0003707; F:steroid hormone receptor activity; IEA.

R GO; GO:0003707; F:steroid hormone receptor activity; IEA.

InterPro; IPR000376; Humon recept 11g.

InterPro; IPR000376; Nucorph receptor.

InterPro; IPR001373; NURR_receptor.

InterPro; IPR001373; Stdfmm receptor.

InterPro; IPR001846; Str_nol_receptor.

InterPro; IPR001846; Str_nol_receptor.

InterPro; IPR001846; Str_nol_receptor.

InterPro; IPR001878; InferPro; IPR001878; INFERPRO
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PRINTS; PRO1284; NUCLEARECPTR.
PRINTS; PRO1284; NUCLEARECPTR.
PRINTS; PRO1289; STROHORNONER.
PRINTS; PRO0399; STROIDFINGER.
ProDom; PD000035; Znf C4steroid; 1.
SMART; SM00399; ZnF C4; 1.
PROSITE; PS00031; NUCLEAR RECEPTOR; 1.
PROSITE; PS00031; Nuclear Protein; Receptor; Transcription; SEQUENCE 586 AA; 65343 MM; 6A91CD8BC0316769 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MPCVOAQYSPSPPGSSYAAQTYS----SEYTTEIMNPDYTKLTMDLGSTEITATATTSLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  160 TSHIMDQQRK-----NAMSRLFSFKQSPVDTPMPSCQMRFDGSLHVSMGPDTA----
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Submitted (JUL-2004) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
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47.6%; Score 1588; DB 2; 1
Best Local Similarity 53.7%; Pred. No. 2.8e-76;
Matches 347; Conservative 74; Mismatches 145;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00104; Hormone recep; 1.
Pfam; PF00105; zf-C4; 1.
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                                                                                                                                                                  VEGYSSNYELKPSCVYQM----QRPLIKVEEGRAPSYHHHHHHHHHHHHQQQQQQDSI 117
                                                                                                                                                                                                       PPASSPEDEVLP-STSMYFKQSPPSTPTTPAFPPQAGALWDEALPSAPGCIAPGPLLDPP 176
                                                                                                                                                                                                                                                               91 QNYVATTHMIEQRKTPVSRLSLPSPKOSPPGTPVSSCOMRFDGPLHVPMNPEPAGSHHV- 149
                                                                                                                                                                                                                                                                                                                           272 GESPSLPSPPSRSSSSGEGTCAVCGDNAACQHYGVRTCEGCKGFFKRTVQKNAKYVCLAN 331
                                                                                                                                                                                                                                                                                                                                                                 KNCPVDKRRRNRCQYCRFQKCLSVGMVKEVVRTDSLKGRRGRLPSKPKSPLQQEPSQPSP 391
                                                                                                                                                                                                                                                                                                                                                                                                       PSPPICMMNALVRALTDSTP--RDLDYSRY-CPTDQAAAGTDAEHVQQFYNLLTASIDVS 448
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PSPPVSLISALVRAHVDSNPAMTSLDYSRRQANPDYQMSGDDTQHIQQFYDLLTGSMEII 354
                                                                                                                                                                                                                  PPQS---EEMMPHSGSVYXKPSSPPTPTTFGFQVQHSPMMDD-----PGSLHNFH 90
                                                                                                                                                                                     ----- 43
                                                                                                                                                                                                                                                                                                -- DIQVPSPPSRGSPSNEGLCAVCGDNAACQHYGVRICEGCKGFFKRIVQKNAKYVCLAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFGEWLDSIKDFSLNLQSLNLDIQALACLSALSMITERHGLKEPKRVEELCNKITSSLKD
                                                                                                                                                                                                                                             177 MKAVPT------PSPAGGHFPLFHFKPSPPHPPA--------PSPAGGHHLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RSWAEKIPGFTDLPKEDQTLLIESAFLELFVLRLSIRSNTAEDKFVFCNGLVLHRLQCLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00011; NUCLEAR_RECEPTOR; 1.
DNA-binding; Metal-binding; Nuclear protein; Receptor; Transcription;
Transcription regulation; Zinc; Zinc-finger.
SEQUENCE 515 AA; 59808 MW; 41CB713EE1192523 CRC64;
                                                                                                                                                                                                                                                                                    213 YDPTAAAALSLPLGAAAAAGSQAAALESHPYGLP-LAKRAAPLAFPPLGLTPSPTASSLL
                                                                                                                                               Gaps
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01-OCT-1996 (Rel. 34, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2014 (Rel. 44, Last annotation update)
Orphan nuclear receptor NR4A1 (Orphan nuclear receptor NGFLB).
Name=NR4A1; Synonyms=HVR;
Canis familiaris (Dog).
                                                                                                                                              102;
                                                                                                                            Length 535;
                                                                                                                                              Indels
                                                                                                                                                                            Query Match
47.1%; Score 1572; DB 2; 1
Best Local Similarity 54.2%; Pred. No. 1.8e-75;
Matches 326; Conservative 63; Mismatches 110;
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        PRINTS; PRO1284; NUCLEARECPTR.
PRINTS; PRO1287; NURMUGCREPTR.
PRINTS; PRO0398; STRDHORNOUR.
PRINTS; PRO0047; STROIDFINGER.
PRODOM; PRO00035; Znf_C4eteroid; 1.
SWART; SM00330; HOLI; 1.
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PF00105;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 ISTFVEGYSSNYELKPSCVYQM---QRPLIKVEEGRAPSYHHHHHHHHHHHHHHHQQQHQQ 114
                                                                                                                                                                                                        B) as an early dog thyrocytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   110 GCYPGPLSGPLDETLSSSGSDYYGSPCSAPSPSTPSFQPPQLSPWDGSFGPFSPSQTYEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MPCVQAQY---SPSPPGSSYAAQTYSSEYTTEIMNPDYTKLTMDLGSTEITATATTSLPS
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                                                                                                                                                                                                  "Induction of nerve growth factor-induced gene-B (NGFI-B) as an ear. event in the cyclic adenosine monophosphate response of dog thyrocyl in primary culture.";
Endocrinology 117:4691-4698(1996).
-i. FUNCTION: Orphan nuclear receptor.
-i. SUBCELLULAR LOCATION: Nuclear.
-i. SUMILARITY: Belongs to the nuclear hormone receptor family. NR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oosphoserine (by PKA) (By similarity) tosphoserine (by PKA) (By similarity) 773563A8EC48F906 CRC64;
Euteleostomi;
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SEQUENCE FROM N.A.
MEDLINE=97050607; PubMed=8895335; DOI=10.1210/en.137.11.4691;
MEDLINE=97050607; PubMed=8895335; DOI=10.1210/en.137.11.4691;
Pichon B., Jimenez-Cervantes C., Pirson I., Maenhaut C.,
Phichon B., Jimenez-Cervantes Fartor-induced gene-B (NGFI-B) as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Score 1371; DB 1; Length 59; Pred. No. 8.6e-65; 81; Mismatches 177; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00031; NŪCLEAR RECEPTOR; 1.
DNA-binding; Nuclear protein; Phosphorýlation; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C4-type.
Ligand-binding (Potential)
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Carnivora, Fissipedia, Canidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nuclear receptor-type
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Phosphoserine
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Poly-Pro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               regulation; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000536; Hrmon_recept_lig.
InterPro; IPR001723; Stdhrmn_receptor.
InterPro; IPR00846; Str.ncl_receptor.
InterPro; IPR001628; Znf_C4steroid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C4-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO0398; STRDHORMONER.
PRINTS; PRO0047; STROLDFINGER.
PROD00M; PD000035; ZRf_C4eteroid; 1.
SMART; SM00430; HOLI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            recep; 1
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Matches 316; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00104; Hormone.
Pfam; PF00105; zf-C4; 1
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598 AA;
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                                                NCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                        subfamily.
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ZN FING
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GCYPGPRSGPVDEALSSSGSDYYGSPCSAPSPSTPSFQPPQLSPWDGSFGHSSPSQTYEG 169
                                                                                                                                                                                                 217 QLG-----EGESYSM-----PTAPPGL----APTSPHLEGSGILDTP-VTSTKARSG 258
                                                                                                                                                                                                                                                                                                    SINLOSINIDIOALACLSALSMITERHGLKEPKRVEELCNKITSSLKDHOSKGQALEPTE 580
                                                          PLIDPPMKAVPTVAGARFPLFHFKPSPPHPPAPSPAGGHHLGYDPTAAAALSL-PLGAAA
                                                                                                           --LRAWTEQLPKASGPPQPPAFFSFSPPTGPSPS-----LAQSPLKLFPSQATH
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MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haleh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=90173205; PubMed=2626032; DOI=10.1016/0022-4731(89)90114-3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
05-AUG-2094 (Rel. 44, Last annotation update)
05-Dhan nuclear receptor NR4A1 (Orphan nuclear receptor HWR)
response protein NAK1) (TR3 orphan receptor).
Name=NR4A1; Synonyms=GFRP1, HWR, NAK1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Fetal skeletal muscle;
MEDLINE=91133413; PubMed=2283997;
Nakai A., Kartha S., Sakurai A., Toback F.G., Degroot L.J.;
"A human early response gene homologous to murine nur77 and
B., and related to the nuclear receptor superfamily.";
Mol. Endocrinol. 4:1438-1443(1990).
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                                                                                                                                                                                      CQYCRFQKCLSVGMVKEVVRTDSLKGRRGRLPSKPKSPLQQEPSQPSPPSPPICMMNALV 403
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                                                                                                              APSGSEGRCAVGGDNASCQHYGVRTCEGCKGFFKRTVQKNAKYICLANKDCPVDKRRRNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A Kochrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
Fobo G., Han M., Wiemann S.;
Fobo G., Han M., Wiemann S.;
Fobo G., Han M., Wiemann S.;
L. Submitted (SEP-2004) to the EMBL/Genbank/DBJ databases.
-1- SUBCELLULAR LOCATION: Nuclear (By similarity).
-1- SIMILARITY: Belongs to the nuclear hormone receptor family.
EMBL; AL81844; CAD38550.2; -.
R GO; 000005634; C:nucleus; IEA.
R GO; 000000700; F:ligand-dependent nuclear receptor activity; IEA.
R GO; 000003700; F:ligand-dependent nuclear receptor activity; IEA.
R GO; 000003700; F:ligand-dependent maclear receptor activity; IEA.
R GO; 0000003700; F:ligand-dependent maclear receptor activity; IEA.
R GO; 0000003700; F:ligand-dependent maclear receptor activity; IEA.
R GO; 0000003700; F:ligand-dependent maclear protein; DNA-binding; Hypothatical protein; Metal-binding; Nuclear protein;
R Receptor; Transcription; Transcription requlation; Zinc; Zinc-finger.
SEQUENCE 598 AA; 64445 MW; C96154E06013AC8B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LPKEDQTLLIESAFLELFVLRLSIRSNTAEDKFVFCNGLVLHRLQCLRGFGEWLDSIKDF
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                                                                                --SSGEGTCAVCGDNAACQHYGVRTCEGCKGFFKRTVQKNAKYVCLANKNCPVDKRRRNR
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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41.0%; Score 1368; DB 2; Length 598;
Best Local Similarity 48.5%; Pred. No. 1.2e-64;
Matches 315; Conservative 80; Mismatches 179; Indels 76;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-UTUN-2003 (TrEMBLrel. 24, Last annotation update)
Hypothetical protein DKFZp451G125.
Name=DKFZp451G125;
                                                                                                                                                                                                                             COPCRFOKCLAVGMVKEVVRTDSLKGRRGRLPSKPKQP-
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TISSUE-Skeletal muscle;
The German cDNA Consortium;
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                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Stankood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.B., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                     -!- INDUCTION: By growth-stimulating agents.
-!- SIMILARITY: Belongs to the nuclear hormone receptor family. NR4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      similarity)
similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor activity; TAS
                                                                                                                                                                                                                                                      -i- SUBCELLUTAR LOCATION: Nuclear.
-i- TISSUE SPECIFICITY: Fetal muscle and adult liver, brain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41.0%; Score 1367; DB 1; Length 598; 47.5%; Pred. No. 1.4e-64; ive 74; Mismatches 165; Indels 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nuclear receptor-type.
C4-type.
C4-type.
Ligand-binding (Potential).
Poly-Ser.
Poly-Pro.
Phosphoserine (by PKA) (By s Phosphoserine (by PKA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00011; NUCLEAR RECEPTOR; 1.
DNA-binding; Nuclear protein; Phosphorylation; Receptor;
Transcription regulation; Zinc-finger.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41DAAEA7C25FDA22 CRC64;
                                                                                                                                                                                                        and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
-!- FUNCTION: Orphan nuclear receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -> P (in Ref. 2).
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GO; GO: 0003677; F: DNA binding; TAS.

GO; GO: 0004879; F: IDNA binding; TAS.

GO; GO: 0004879; F: Ignand-dependent nuclear rec

GO; GO: 0004879; F: Ignand-transduction; TAS.

InterPro; IPRO01723; F: Eddram receptor.

InterPro; IPRO01723; F: Ctdram receptor.

InterPro; IPRO01824; Stchram receptor.

InterPro; IPRO01829; Stchram receptor.

InterPro; IPRO01829; Stchram receptor.

InterPro; IPRO01829; Zrf-C44; I.

PRINTS; PRO0195; Zf-C4; I.

PRINTS; PRO0199; STRDIDFINGER.

PROD047; STROIDFINGER.

PROD047; STROIDFINGER.

PROM0410; HOIL; I.

SMART; SM00399; ZRF C4; I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC016147; AAH16147.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSFAC; T02767; -.
Genew; HGNC:7980; NR4A1.
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459
92
341
351
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HSSP; P43354; 10VL.
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370
598 AA;
                                                                                                                                                                                                                                                                                                                                     subfamily.
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MOD_RES
CONFLICT
CONFLICT
SEQUENCE
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23;

Gaps

Indels 112;

Conservative

Best Local Similarity Matches 317; Conserv

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385
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                                                                                                                                              58 ISTFVEGYSSNYELKPSCVYQMQ---RPLIKVEEGRAPSYHHHHHHHHHHHHHHQQQHQQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         242 GSGILDTP-VTSTKARSGAPGGSEGRCAVCGDNASCQHYGVRTCEGCKGFFKRTVQKNAK
                                              110 GCYPGPLSGPVDEALSSSGSDYYGSPCSAPSPSTTPSFQPPQLSPWDGSFGHFSPSQTYEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G----ESPSLPSPPSRSSSSG--EGTCAVCGDNAACQHYGVRTCEGCKGFFKRTVQKNAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53 FSTFMDGYTGEFD----TFLYQLPGTVQPCSSASSSASSTSSSSATSPASASFKFEDFQVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                  154 -ALWDEALPSAPGCIAPGPLLDPPMKAVPTVAGARFPLFHFKPSPPHPPAPSPAGGHHLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                213 YDPTAAAALSL-PLGAAAAAGSQAAALESHPYGLPLAKRAAPLAFPPLGLTPSPTASSLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YVCLANKNCPVDKRRRNRCQYCRFQKCLSVGMVKEVVRTDSLKGRRGRLPSKPKSPLQQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSQPSPPSPPICMMNALVRALTDSTP--RDLDYSRYCPTDQAAAG-TDAEHVQQFYNLLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ASIDVSRSWAEKIPGFTDLPKEDQTLLIESAFLELFVLRLSIRSNTAEDKFVFCNGLVLH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LRAWTEQLPKASG------PPQ------PPAFFSFSPPTGPSPS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLQCLRGFGEWLDSIKDFSLNLQSLNLDIQALACLSALSMITERHGLKEPKRVEELCNKI
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Catarrhini; Hominidae; Homo.
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Ebert L., Schick M., Neubert P., Schatten R., Henze S., Korn B. Submitted (JUN-2004) to the EMBL/GenBank/DDBJ databases.

-1 - SUBJCELLULAR LOCATION: Unclear (By similarity)

-1 - SINILARITY: Belongs to the nuclear hormone receptor family. EMBL; CR456704; CAG32985.1; -.

HSSP; P20393; JA6Y.

GO, GO:000534; C:nucleus; IEA.

GO, GO:0003707; F:steroid hormone receptor activity; IEA.

GO: GO:0003700; F:transcription factor activity; IEA.
                                                                                                                                                                                                                                                                                                115 PSIP-PASSPEDEVLPSTSMYFKQSPPS--TPTTPAF-PPQAG-----
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Last sequence update)
Last annotation update)
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Eukaryota, Metazoa, Chordata,
Mammalia, Eutheria, Primates,
NCBI_TaxID=9606;
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IFMDTLPF
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05-JUL-2004
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06 1818
1D Q6 1818
AC Q6 1810
DT 05-JU
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 ISTFVEGYSSNYELKPSCVYQMQ---RPLIKVEEGRAPSYHHHHHHHHHHHHQQQHQQ 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 -ALWDEALPSAPGCIAPPGPLLDPPMKAVPTVAGARFPLFHFKPSPPHPPAPSPAGGHHLG 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202 ---LAQSPLKLFPSQATHQLG-----5GESYSM------PTAFPGL----APTSPHLE 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              272 G----ESPSLPSPPSRSSSG--EGTCAVCGDNAACQHYGVRTCEGCKGFFKRTVQKNAK 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               326 YVCLANKNCPVDKRRRNRCQYCRPQKCLSVGMVKEVVRTDSLKGRRGRLPSKPKSPLQQE 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      386 PSQPSPPSPPICMMNALVRALIDSTP--RDLDYSRYCPTDQAAAG-TDAEHVQQFYNLLT 442
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411
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                                                                                                                                                                                                                                                          PRINTS; PRO1285; HNRNUCRECPTR.
PRINTS; PRO1285; HNRNUCRECPTR.
PRINTS; PRO1286; STRDHORNONER.
PRINTS; PRO0398; STRDHORNONER.
PRINTS; PRO0039; DATE C48teroid; 1.
SMART; SM00430; HOLI_1.
SMART; SM00430; HOLI_1.
SMART; SM00430; HOLI_2.
SMART; HOLI_2.
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GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 40.9%; Score 1364; DB 2; Length 598; Best Local Similarity 47.5%; Pred. No. 2e-64; Matches 317; Conservative 74; Mismatches 165; Indels 112;
                         InterPro; IPR003071; HMR_receptor.
InterPro; IRR000536; Hrmon_recept_lig.
InterPro; IRR001723; Stdhrmn receptor.
InterPro; IPR001723; Stdhrmn receptor.
InterPro; IPR008946; Str_ncl_receptor.
InterPro; IPR001628; Ztr_ncl_receptor.
Pfam; PF00104; Hormone_recept_l
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591 IFMDTLPF 598
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